

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 20, 2005, 15:14:10 ; Search time 75 Seconds  
(without alignments)  
2346.346 Million cell updates/sec

Title: US-10-622-201-70

Perfect score: 2288  
Sequence: 1 MLHGASRRPARKSSGLSG.....FMDIAGLGAKIELSDTKA 455

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp19808:\*  
2: geneseqp19908:\*  
3: geneseqp20008:\*  
4: geneseqp20018:\*  
5: geneseqp20028:\*  
6: geneseqp20038:\*  
7: geneseqp20038:\*  
8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2288	100.0	455	2	AAR26449 CP4-EPSPS
2	2288	100.0	455	2	AAW39426 CP4-EPSPS
3	2288	100.0	455	7	AAE39920 Class II
4	2288	100.0	455	8	ADJ79608 A_tumefac
5	2288	100.0	527	4	AAW52214 EPSPS SEQ
6	2282	99.7	455	2	AAR22300 Class II
7	2282	99.7	455	2	AAW24474 Class II
8	2282	99.7	455	2	AAW24474 Class II
9	2282	99.7	455	2	AAW71609 Agrobacte
10	2282	99.7	455	4	AAE05053 Agrobacte
11	2282	99.7	455	6	AAE31621 5-Enolpyr
12	2282	99.7	455	7	AAE39899 Agrobacte
13	1900.5	83.1	449	2	AAR22301 Class II
14	1900.5	83.1	449	2	AAR22302 Class II
15	1900.5	83.1	449	2	AAW34685 Class II
16	1900.5	83.1	449	2	AAW34684 Class II
17	1900.5	83.1	449	2	AAW24480 Class II
18	1900.5	83.1	449	2	AAW24479 Class II
19	1900.5	83.1	449	2	AAW71611 Pseudomon
20	1900.5	83.1	449	2	AAW71610 Pseudomon
21	1900.5	83.1	449	4	AAE05055 Pseudomon
22	1900.5	83.1	449	4	AAE05054 Achromoba
23	1900.5	83.1	449	7	AAE39901 Pseudomon
24	1900.5	83.1	449	7	AAE39901 Pseudomon
25	1783	77.9	452	8	ADS23083 Bacterial

26	1233.5	53.9	430	8	ADS42336	Ads42336 Bacterial
27	1213.5	53.0	432	8	ADS21443	Ads21443 Bacterial
28	1188.5	51.9	418	8	ADN25161	Adn25161 Bacterial
29	1149.5	50.2	420	8	ADS29006	Ads29006 Bacterial
30	1135	49.6	443	8	ADS28041	Ads28041 Bacterial
31	989.5	43.2	782	7	ABO72808	AbO72808 Pseudomon
32	983	43.0	411	8	ADN27321	Adn27321 Bacterial
33	961.5	42.0	758	6	ADA33234	Ada33234 Acinetoba
34	927.5	40.5	442	8	ADS26350	Ads26350 Bacterial
35	912.5	39.9	454	8	ADS28697	Ads28697 Bacterial
36	908.5	39.7	408	8	ADN26649	Adn26649 Bacterial
37	908.5	39.7	412	8	ADN26846	Adn26846 Bacterial
38	906.5	39.6	408	8	ADS26718	Ads26718 Bacterial
39	906.5	39.6	408	8	ADS27102	Ads27102 Bacterial
40	902.5	39.4	773	8	ADL05904	Adl05904 M. catarr
41	884	38.6	431	8	ADS28209	Ads28209 Bacterial
42	878	38.4	675	8	ADS24901	Ads24901 Bacterial
43	867.5	37.9	447	2	AAW34688	AAW34688 Class II
44	867.5	37.9	447	2	AAW24487	AAW24487 Class II
45	867.5	37.9	447	2	AAW71619	AAW71619 Synechocy

## ALIGNMENTS

RESULT 1  
AAR26449  
ID AAR26449 standard; protein; 455 AA.  
XX  
AC AAR26449;  
XX  
DT 25-MAR-2003 (revised)  
DT 28-JAN-1993 (first entry)  
XX  
XX CP4-EPSPS.  
DE  
XX PMON11030; CTP2; CP4; EPSPS; chloroplast transit peptide;  
XX 5-enolpyruvyl-3-shikimate phosphate synthetase; ACC; ethylene;  
XX Pseudomonas chloroaphis 6G5.  
OS  
XX Synthetic.  
XX  
XX W09212249-A1.  
XX  
PD 23-JUL-1992.  
XX  
XX 17-DEC-1991; 91WO-US009437.  
XX  
XX 26-DEC-1990; 90US-00632440.  
XX  
XX (MONS ) MONSANTO CO.  
XX  
XX Klee HJ, Kishore GM;  
XX WPI; 1992-284334/34.  
XX N-FSDB; AAQ27201.  
XX  
XX Delaying fruit ripening and senescence in plants - by controlling  
XX ethylene@ prodn., pref. by expression of 1-amino-cyclopropane-1-  
XX carboxylic acid deaminase.  
XX  
XX Disclosure; Page 64-66; 110pp; English.  
XX  
XX The sequences given in AAR26448 and AAR26449 are encoded by genes which  
XX were used in the construction of an expression plasmid pMON11030 which  
XX was used to transform petunia plants. This plasmid contained the genes  
XX for chloroplast transit peptide (CTP2) (AAR26448) and the CP4 synthetase 5  
XX -enolpyruvyl-3-shikimate phosphate synthetase (EPSPS) gene (AAR26449)  
XX which is capable of conferring resistance to glyphosate. The plasmid also  
XX contained the 1-aminocyclo-propane-1-carboxylic acid (ACC) deaminase gene  
XX from Pseudomonas chloroaphis (see also AAQ27199). The transformed plants  
XX had ethylene levels reduced to about one half that of the control,  
XX untransformed plants. It is expected that such plants will show reduced

CC senescence of flowers and leaves when compared to untransformed plants.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX  
 SQ Sequence 455 AA;

Query Match 100.0%; Score 2288; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-180; Mismatches 0; Indels 0; Gaps 0;  
 Matches 455; Conservative 0;

QY 1 MLHGASSRPATARKSSGSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
 |||||  
 DB 1 MLHGASSRPATARKSSGSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
 QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLDPGNAATGCRITMGLVGYDFDSTFI 120  
 |||||  
 DB 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLDPGNAATGCRITMGLVGYDFDSTFI 120  
 QY 121 GPASLTKRPMGVNLPLREMGVQVKSSEDGRPLVTLRGPKTPTPTTYRVPMAAQAQVKSAY 180  
 |||||  
 DB 121 GPASLTKRPMGVNLPLREMGVQVKSSEDGRPLVTLRGPKTPTPTTYRVPMAAQAQVKSAY 180  
 QY 181 LLAGINTGCTTIVIEPIIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGSKLTGQYID 240  
 |||||  
 DB 181 LLAGINTGCTTIVIEPIIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGSKLTGQYID 240  
 QY 241 VPGDSSSTAFPLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSD 300  
 |||||  
 DB 241 VPGDSSSTAFPLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSD 300  
 QY 301 VADLVRSSSTLKGVTVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLLELRVKESDRLSA 360  
 |||||  
 DB 301 VADLVRSSSTLKGVTVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLLELRVKESDRLSA 360  
 QY 361 VANGLKLVGDCDEGETSLVVRGPDGKGLGNASGAAVAATHLDRHIAVSFLVMGLVSENP 420  
 |||||  
 DB 361 VANGLKLVGDCDEGETSLVVRGPDGKGLGNASGAAVAATHLDRHIAVSFLVMGLVSENP 420  
 QY 421 VTVDATMTATSPPEFMDLMAGLGAKEIELSDTKAA 455  
 |||||  
 DB 421 VTVDATMTATSPPEFMDLMAGLGAKEIELSDTKAA 455

## RESULT 2

AAW39426  
 ID AAW39426 standard; protein; 455 AA.

AC AAW39426;  
 XX  
 DT 19-MAY-1998 (first entry)  
 DE CP4-EPSPS protein.  
 XX  
 KW 1-aminocyclopropane-1-carboxylic acid deaminase; ACC deaminase;  
 KW fruit ripening; ethylene production; glyphosate resistance;  
 KW 5-enolpyruvyl-3-shikimate phosphatase synthase; EPSPS; CP4.  
 XX  
 OS Synthetic.  
 XX  
 PN US5702933-A.  
 XX  
 PD 30-DEC-1997.  
 XX  
 PF 06-NOV-1995; 95US-00553943.  
 XX  
 PR 26-DEC-1990; 90US-00632440.  
 PR 17-DEC-1991; 91US-00809457.  
 XX  
 PA (MONS ) MONSANTO CO.  
 XX  
 PI Klee HJ, Kishore GM;  
 XX  
 DR WPI: 1998-076419/07.  
 DR N-PSDB; AAV09719.

XX Production of plants with delayed ripening - using DNA encoding 1-  
 PT amino:cyclo:propane-1-carboxylic acid deaminase.  
 XX  
 XX  
 PS  
 XX Example 9; Fig 21; 56pp; English.

CC This sequence represents the synthetic CP4 5-enolpyruvyl-3-shikimate  
 CC phosphate synthase (EPSPS) gene which is capable of conferring resistance  
 CC to glyphosate and is used in a novel method for producing fruit-bearing  
 CC plants with delayed ripening. The method involves the expression of a 1-  
 CC aminocyclopropane-1-carboxylic acid (ACC) deaminase gene in a plant at a  
 CC level sufficient to reduce ethylene production in the fruit

XX Sequence 455 AA;

Query Match 100.0%; Score 2288; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-180; Mismatches 0; Indels 0; Gaps 0;  
 Matches 455; Conservative 0;

QY 1 MLHGASSRPATARKSSGSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
 |||||  
 DB 1 MLHGASSRPATARKSSGSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
 QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLDPGNAATGCRITMGLVGYDFDSTFI 120  
 |||||  
 DB 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLDPGNAATGCRITMGLVGYDFDSTFI 120  
 QY 121 GPASLTKRPMGVNLPLREMGVQVKSSEDGRPLVTLRGPKTPTPTTYRVPMAAQAQVKSAY 180  
 |||||  
 DB 121 GPASLTKRPMGVNLPLREMGVQVKSSEDGRPLVTLRGPKTPTPTTYRVPMAAQAQVKSAY 180  
 QY 181 LLAGINTGCTTIVIEPIIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGSKLTGQYID 240  
 |||||  
 DB 181 LLAGINTGCTTIVIEPIIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGSKLTGQYID 240  
 QY 241 VPGDSSSTAFPLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSD 300  
 |||||  
 DB 241 VPGDSSSTAFPLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSD 300  
 QY 301 VADLVRSSSTLKGVTVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLLELRVKESDRLSA 360  
 |||||  
 DB 301 VADLVRSSSTLKGVTVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLLELRVKESDRLSA 360  
 QY 361 VANGLKLVGDCDEGETSLVVRGPDGKGLGNASGAAVAATHLDRHIAVSFLVMGLVSENP 420  
 |||||  
 DB 361 VANGLKLVGDCDEGETSLVVRGPDGKGLGNASGAAVAATHLDRHIAVSFLVMGLVSENP 420  
 QY 421 VTVDATMTATSPPEFMDLMAGLGAKEIELSDTKAA 455  
 |||||  
 DB 421 VTVDATMTATSPPEFMDLMAGLGAKEIELSDTKAA 455

## RESULT 3

AAE39920  
 ID AAE39920 standard; protein; 455 AA.

AC AAE39920;  
 XX  
 DT 18-DEC-2003 (first entry)  
 DE Class II EPSPS enzyme related protein.  
 XX  
 KW Glyphosate tolerant 5-enolpyruvylshikimate-3-phosphate synthase; enzyme;  
 KW transgenic plant; transgenic; herbicide; weed control; EPSPS.  
 XX  
 OS Unidentified.  
 XX  
 PN US2002168680-A1.  
 XX  
 PD 14-NOV-2002.  
 XX  
 PF 16-DEC-1999; 99US-00464099.  
 XX

PR 31-AUG-1990; 90US-00576537.  
PR 28-AUG-1991; 91US-00749611.  
PR 13-SEP-1994; 94US-00306063.  
PR 07-APR-1997; 97US-00833485.  
PR 20-AUG-1998; 98US-00137440.  
XX (BARR/) BARRY G F.  
PA (KISH/) KISHORE G M.  
PA (PADG/) PADGETTE S R.  
PA (STLL/) STALLINGS W C.  
XX  
XX Barry GF, Kishore GM, Padgette SR, Stallings WC;  
XX WPI: 2003-719984/68.  
XX  
XX New 5-enolpyruvylshikimate-3-phosphate synthase DNA sequence useful for  
PT producing genetically transformed plants, and selectively controlling  
PT weeds in a field containing crop having planted crop seeds or plants.  
XX  
XX Disclosure: Page 82-83; 158pp; English.  
XX  
XX The invention relates to glyphosate tolerant 5-enolpyruvylshikimate-3  
CC phosphate synthase (EPSPS) enzymes and nucleic acid molecules encoding  
CC such enzymes. The invention is useful for producing genetically  
CC transformed plants which are tolerant to a glyphosate herbicide and for  
CC selectively controlling weeds in a field containing a crop having planted  
CC crop seeds or plants. The present sequence is a protein related to the  
CC invention  
XX  
XX Sequence 455 AA;  
SQ

Query Match 100.0%; Score 2288; DB 7; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.2e-180;  
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLHGASSRPRATARKSSGSGTIRIPGDKSISHSRFMGGLASGETRITGLGEGEDVINTG 60  
DB 1 MLHGASSRPRATARKSSGSGTIRIPGDKSISHSRFMGGLASGETRITGLGEGEDVINTG 60  
QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNATGRLTMGLVGYVDFDSTFI 120  
DB 61 KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNATGRLTMGLVGYVDFDSTFI 120  
QY 121 GNASLTKRMGRVNLPLREMGVQVKSDEDDRLPVTLRGKPTPTITRYVPMASAOVKSAY 180  
DB 121 GNASLTKRMGRVNLPLREMGVQVKSDEDDRLPVTLRGKPTPTITRYVPMASAOVKSAY 180  
QY 181 LLAGLNTPGITTVIBIMTRDHTERKMLQGFGANLTVETDADGVRTIRLGRGLTGQVID 240  
DB 181 LLAGLNTPGITTVIBIMTRDHTERKMLQGFGANLTVETDADGVRTIRLGRGLTGQVID 240  
QY 241 VEGDPSSTAFPLVAALLVPGSDVTILNVLNMPRTGLIITLQMGADIEVINPRLAGGED 300  
DB 241 VEGDPSSTAFPLVAALLVPGSDVTILNVLNMPRTGLIITLQMGADIEVINPRLAGGED 300  
QY 301 VADLRRSSTLKGVTYPERAPSMIDERYIILAVAAFAAGATYMGLEELRYKESRLSA 360  
DB 301 VADLRRSSTLKGVTYPERAPSMIDERYIILAVAAFAAGATYMGLEELRYKESRLSA 360  
QY 361 VANGKLNVDCDEGETSLVVRGPRPGKIGNAGSAVAATHLDRIRAMSFVLWGLVSENP 420  
DB 361 VANGKLNVDCDEGETSLVVRGPRPGKIGNAGSAVAATHLDRIRAMSFVLWGLVSENP 420  
QY 421 VTVDATMTATSPFERMDLMAIGAKIELSDTKAA 455  
DB 421 VTVDATMTATSPFERMDLMAIGAKIELSDTKAA 455

RESULT 4  
ADJ79608 standard; protein; 455 AA.  
XX  
AC ADJ79608;

XX 06-MAY-2004 (first entry)  
DT A\_tumefaciens EPSPS protein modified to be glyphosate resistant Segid15.  
XX  
DE  
XX EPSPS; glyphosate resistant; enolpyruvyl-3-phosphoshikimate synthase;  
XX transgene silencing; transgenic; plant; agronomical phenotype;  
KW drought tolerance; cold tolerance; herbicide tolerance; yield;  
KW disease resistance; insect resistance; genetic engineering.  
XX  
OS Agrobacterium tumefaciens.  
OS Synthetic.  
XX  
XX WO2004009761-A2.  
XX  
XX 29-JAN-2004.  
XX  
XX 10-JUL-2003; 2003WO-US021551.  
XX  
XX 18-JUL-2002; 2002US-0396665P.  
XX  
XX (MONS ) MONSANTO TECHNOLOGY LLC.  
XX  
XX Flaeinski S;  
XX  
XX WPI: 2004-132939/13.  
DR N-PSDB; ADJ79609, ADJ79610, ADJ79611, ADJ79616.  
XX  
XX Reducing transgene silencing with artificial polynucleotides, useful in  
PT producing commercial transgenic plants having increased herbicide  
PT tolerance, insect resistance, drought tolerance, cold tolerance and  
PT disease resistance.  
XX  
XX Example 4; SEQ ID NO 15; 162pp; English.  
XX

CC This invention relates to novel methods for constructing artificial  
CC polynucleotides and ways to reduce transgene silencing in transgenic  
CC plants. Specifically, it refers to introducing an artificial  
CC polynucleotide that is divergent from an endogenous plant gene, but which  
CC encodes a substantially identical protein. The present invention  
CC describes artificial polynucleotides that encode proteins with an  
CC agronomically useful phenotype, such as drought, cold or herbicide  
CC tolerance, increased yield and disease or insect resistance. In  
CC particular, it refers to a modified enolpyruvyl-3-phosphoshikimate  
CC synthase (EPSPS) enzyme required for the synthesis of aromatic amino  
CC acids, which is resistant to the phytotoxic herbicide glyphosate.  
CC Accordingly, these methods and compositions are useful for plant genetic  
CC engineering to produce commercially viable transgenic plants with  
CC improved agronomical phenotypes. This polypeptide sequence is an  
CC agrobacterium tumefaciens strain CP4 EPSPS protein modified to be  
CC glyphosate resistant with chloroplast transit peptide, given in an  
CC exemplification of the invention.  
XX  
XX Sequence 455 AA;  
SQ

Query Match 100.0%; Score 2288; DB 8; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.2e-180;  
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLHGASSRPRATARKSSGSGTIRIPGDKSISHSRFMGGLASGETRITGLGEGEDVINTG 60  
DB 1 MLHGASSRPRATARKSSGSGTIRIPGDKSISHSRFMGGLASGETRITGLGEGEDVINTG 60  
QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNATGRLTMGLVGYVDFDSTFI 120  
DB 61 KAMQAMGARIRKEGDTWIIDGVNGGLLAPEAPLDFGNATGRLTMGLVGYVDFDSTFI 120  
QY 121 GNASLTKRMGRVNLPLREMGVQVKSDEDDRLPVTLRGKPTPTITRYVPMASAOVKSAY 180  
DB 121 GNASLTKRMGRVNLPLREMGVQVKSDEDDRLPVTLRGKPTPTITRYVPMASAOVKSAY 180  
QY 181 LLAGLNTPGITTVIBIMTRDHTERKMLQGFGANLTVETDADGVRTIRLGRGLTGQVID 240  
DB 181 LLAGLNTPGITTVIBIMTRDHTERKMLQGFGANLTVETDADGVRTIRLGRGLTGQVID 240

Db 181 LLAGNTPGITTVIEPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGKLTGVYID 240  
QY 241 VPGDPSSTAFPLVALLVPGSDVTILNVLMNPTRTGLITLTQEMGADIEVINPRLAGGED 300  
Db 241 VPGDPSSTAFPLVALLVPGSDVTILNVLMNPTRTGLITLTQEMGADIEVINPRLAGGED 300  
QY 301 VADLRVRSTLKGTVVPEDRAPSMIDEPYIILAVAAAFAGATVMNGLEELRYKESDRISA 360  
Db 301 VADLRVRSTLKGTVVPEDRAPSMIDEPYIILAVAAAFAGATVMNGLEELRYKESDRISA 360  
QY 361 VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAYATHLDRHRIAMSFVLMGLVSENP 420  
Db 361 VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAYATHLDRHRIAMSFVLMGLVSENP 420  
QY 421 VTVDATMIATSFPEFMDLMAGLGAKEIISDTKAA 455  
Db 421 VTVDATMIATSFPEFMDLMAGLGAKEIISDTKAA 455

## RESULT 5

AAMS2214  
ID AAMS2214 standard; protein; 527 AA.

AC AAMS2214;

DT 11-SEP-2003 (revised)  
DT 12-FEB-2002 (first entry)

DE EPSPS SEQ ID NO 3.

XX Transgenic plant; herbicide resistance; EPSPS; GOX; Petunia hybrida;  
KM 5-enolpyruvylshikimate-3-phosphate synthase; glyphosate oxidoreductase;  
KW protoporphyrinogen IX oxidase; immunoglobulin; Agrobacterium; strain CP4;  
KM chloroplast transit peptide.

OS Petunia x hybrida.  
OS Agrobacterium sp.

PN JP2001190168-A.

XX 17-JUL-2001.

PF 27-OCT-2000; 2000JP-00328811.

PR 29-OCT-1999; 99JP-00310244.

PA (SUMO ) SUMITOMO CHEM CO LTD.

DR WPI; 2001-605307/69.

DR N-PSDB; ABA02854.

XX New herbicide-resistant plant.

PS Example; Page 46-48; 66pp; Japanese.

XX The invention relates to a transgenic plant which shows resistance to a  
CC herbicide in an amount inhibiting natural 5-enolpyruvylshikimate-3-  
CC phosphate synthase (EPSPS) activity of the plant and having at least one  
CC enzymatic activity selected from: (1) EPSPS activity different from  
CC natural EPSPS activity of the plant or (2) glyphosate oxidoreductase  
CC (GOX) activity different from the natural GOX activity of the plant; and  
CC in which a gene encoding a protein having the following properties: (a)  
CC combines specifically with a substance participating to the herbicidal  
CC activity a herbicide of protoporphyrinogen IX oxidase inhibiting type;  
CC (b) has substantially no denaturing activity on a substance to which said  
CC protein combines specifically; and (c) contains substantially no  
CC framework region of the variable region of immunoglobulin. The present  
CC sequence is that of the Petunia hybrida EPSPS chloroplast transit peptide  
CC and the Agrobacterium sp. strain CP4 EPSPS gene. (Updated on 11-SEP-2003  
CC to standardise OS field)

XX Sequence 527 AA;

Query Match 100.0%; Score 2288; DB 4; Length 527;  
Best Local Similarity 100.0%; Pred. No. 1,4e-180;  
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLHGASSPATARSSGSGVTRIPGDKSISHRSFMFGLASGETRTGLLEGEDVINTG 60  
Db 73 MLHGASSPATARSSGSGVTRIPGDKSISHRSFMFGLASGETRTGLLEGEDVINTG 132  
QY 61 KAMQMGARIRKEGDTWIIDGVNGGLIAPAPLDFGNAATGCRITMGLVGVDSTFI 120  
Db 133 KAMQMGARIRKEGDTWIIDGVNGGLIAPAPLDFGNAATGCRITMGLVGVDSTFI 192  
QY 121 GDASTKPKMRVYNPLREMGVQVSEGDRLPTLRPKPTPTPTTYVPMASAVKSAV 180  
Db 193 GDASTKPKMRVYNPLREMGVQVSEGDRLPTLRPKPTPTPTTYVPMASAVKSAV 252  
QY 181 LLAGNTPGITTVIEPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGKLTGVYID 240  
Db 253 LLAGNTPGITTVIEPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGKLTGVYID 312  
QY 241 VPGDPSSTAFPLVALLVPGSDVTILNVLMNPTRTGLITLTQEMGADIEVINPRLAGGED 300  
Db 313 VPGDPSSTAFPLVALLVPGSDVTILNVLMNPTRTGLITLTQEMGADIEVINPRLAGGED 372  
QY 301 VADLRVRSTLKGTVVPEDRAPSMIDEPYIILAVAAAFAGATVMNGLEELRYKESDRISA 360  
Db 373 VADLRVRSTLKGTVVPEDRAPSMIDEPYIILAVAAAFAGATVMNGLEELRYKESDRISA 432  
QY 361 VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAYATHLDRHRIAMSFVLMGLVSENP 420  
Db 433 VANGKLNGVDCDEGETSLVVRGRPDGKGLGNASGAAYATHLDRHRIAMSFVLMGLVSENP 492  
QY 421 VTVDATMIATSFPEFMDLMAGLGAKEIISDTKAA 455  
Db 493 VTVDATMIATSFPEFMDLMAGLGAKEIISDTKAA 527

## RESULT 6

AAR22300  
ID AAR22300 standard; protein; 455 AA.

AC AAR22300;

DT 24-OCT-2003 (revised)  
DT 03-AUG-1992 (first entry)

DE Claes II EPSPS enzyme.

KM Glyphosate tolerant bacteria; herbicides; glyphosate resistant plants;  
KW 5'-enolpyruvylshikimate-3-phosphate synthase; weed control.

OS Agrobacterium sp; strain CP4.

PN WO9204449-A.

XX 19-MAR-1992.

PF 28-AUG-1991; 91WO-US006148.

PR 31-AUG-1990; 90US-00576537.

PA (MONS ) MONSANTO CO.

DR Barry GF, Kishore GM, Padgett SR;

DR WPI; 1992-114356/14.

XX DNA encoding Claes II 5'-enolpyruvyl shikimate-3-phosphate synthase - for  
PT producing plants and bacteria tolerant to glyphosate herbicides.  
XX Disclosure; Fig 3; 148pp; English.

XX The sequence is that of the Class II 5'-enolpyruvylshikimate-3 phosphate

CC synthase enzyme (EPSPS) of *Agrobacterium* sp. strain CP4. It is used to  
 CC create glyphosate resistant plants or seeds which can be planted in a  
 CC field of crops to selectively control weeds. The crops selected for are  
 CC e.g. corn, wheat, rice, oilseed rape, tobacco and alfalfa. This provides  
 CC a cost effective, environmentally compatible weed control device. See  
 CC also AAM23301 and AAM23302. (Updated on 24-OCT-2003 to standardise OS  
 CC field)  
 CC XX  
 CC XX  
 SQ Sequence 455 AA;  
 Query Match 99.7%; Score 2282; DB 2; Length 455;  
 Best Local Similarity 99.8%; Pred. No. 3.6e-180;  
 Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MSHGASSRPATARKSSGSLGTVRIPEDKSIHSRSFMEGLASGETRTITLGEEDVYING 60  
 DB 1 MSHGASSRPATARKSSGSLGTVRIPEDKSIHSRSFMEGLASGETRTITLGEEDVYING 60  
 QY 61 KAMQAMGARIRKEGDTWIIDVGNGLAPAPLDFGNATGCRITMGLVGYDFDSTFI 120  
 DB 61 KAMQAMGARIRKEGDTWIIDVGNGLAPAPLDFGNATGCRITMGLVGYDFDSTFI 120  
 QY 121 GDSILTKRPMGVLNPLREMGVQVXSEDDRLPVTLRGKPTPTPIYRVPMASQVKSAY 180  
 DB 121 GDSILTKRPMGVLNPLREMGVQVXSEDDRLPVTLRGKPTPTPIYRVPMASQVKSAY 180  
 QY 181 LLAGINTPGITTVIPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGRKLTGQVID 240  
 DB 181 LLAGINTPGITTVIPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGRKLTGQVID 240  
 QY 241 VPGDPSSTAFPLVAALLVGS DVTILNVLNMPTRTGLITLQEMGADIVINPRLAGSD 300  
 DB 241 VPGDPSSTAFPLVAALLVGS DVTILNVLNMPTRTGLITLQEMGADIVINPRLAGSD 300  
 QY 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYILAFAAGATVMNGLEELRYKESDRLSA 360  
 DB 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYILAFAAGATVMNGLEELRYKESDRLSA 360  
 QY 361 VANGKLKNGVDDEGTSIVNVRGPRPGKLGNAAGAAVTHDRIAMSFVWGLVSENP 420  
 DB 361 VANGKLKNGVDDEGTSIVNVRGPRPGKLGNAAGAAVTHDRIAMSFVWGLVSENP 420  
 QY 421 VTVDATMTATSPPEFMDMAGIAGKIELSDTKAA 455  
 DB 421 VTVDATMTATSPPEFMDMAGIAGKIELSDTKAA 455  
 RESULT 7  
 AAM34683  
 ID AAM34683 standard; protein; 455 AA.  
 AC AAM34683;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 17-FEB-1998 (first entry)  
 XX  
 DE Class II EPSP synthase (EPSPS) from *Agrobacterium* sp. strain CP4.  
 XX  
 KW 5-enolpyruvylshikimate-3-phosphate synthase; EPSPS; glyphosate;  
 KW shikimate acid pathway; phosphoenolpyruvic acid; 3-phosphoshikimic  
 KW 5-enolpyruvyl-3-phosphoshikimic acid; herbicide; transgenic plant;  
 KW glyphosate resistance gene; glyphosate-tolerance; promoter.  
 XX  
 OS *Agrobacterium* sp; strain CP4.  
 XX  
 FH Key Location/Qualifiers  
 FT 26..29  
 FT /label= characteristic\_region  
 FT /note="see AAM34691"  
 FT Region 173..177  
 FT /label= characteristic\_region  
 FT /note="see AAM34692"  
 FT Region 200..204

FT /label= characteristic\_region  
 FT /note="see AAM34690"  
 FT 271..274  
 FT /label= characteristic\_region  
 FT /note="see AAM34693"  
 XX  
 XX  
 PN US5627061-A.  
 XX  
 PD 06-MAY-1997.  
 XX  
 PF 07-JUN-1995; 95US-00476008.  
 XX  
 PR 31-AUG-1990; 90US-00576537.  
 PR 28-AUG-1991; 91US-00749611.  
 PR 13-SEP-1994; 94US-00306063.  
 XX  
 PA (MONS ) MONSANTO CO.  
 XX  
 PI Stallings WC, Padgett SR, Kishore GM, Barry GF;  
 XX  
 DR WPI: 1997-271315/24.  
 DR N-PSDB; AAT93788.  
 XX  
 PT Production of glyphosate-herbicide tolerant plants - using DNA encoding  
 PT class II 5-enolpyruvylshikimate-3-phosphate synthase enzyme(s).  
 XX  
 PS Claim 7, Fig 3; 151pp; English.  
 XX  
 CC AAM34683-89 represent a new class of glyphosate-tolerant 5-  
 CC enolpyruvylshikimate-3-phosphate synthases (EPSPS). These novel EPSPS  
 CC enzymes have little homology with known Class I EPSPS enzymes, and belong  
 CC to a new class, Class II. The present sequence is from *Agrobacterium* sp.  
 CC strain CP4. The EPSPS enzymes are part of the shikimic acid pathway,  
 CC which leads to the biosynthesis of aromatic compounds. EPSPS converts  
 CC phosphoenolpyruvic acid (PEP) and 3-phosphoshikimic acid to 5-enolpyruvyl  
 CC -3-phosphoshikimic acid, and is inhibited by the herbicide glyphosate. It  
 CC would be useful to produce transgenic crops containing glyphosate  
 CC resistance genes so that glyphosate-containing herbicides can be applied  
 CC to selectively kill weeds. The novel EPSPS enzymes exhibit a low Km for  
 CC PEP and a high Ki for glyphosate, such that when introduced into a plant,  
 CC the plant is made glyphosate-tolerant, and EPSPS enzyme activity is not  
 CC affected. These class II EPSPS enzymes are fused to a chloroplast transit  
 CC peptide to target the protein into the chloroplast, which is the site for  
 CC the shikimic acid pathway. In addition, the EPSPS gene is cloned into a  
 CC plant under the control of a promoter such as figwort mosaic virus  
 CC promoter or the cauliflower mosaic virus promoter, so that expression is  
 CC enhanced. (Updated on 17-OCT-2003 to standardise OS field)  
 CC XX  
 SQ Sequence 455 AA;  
 Query Match 99.7%; Score 2282; DB 2; Length 455;  
 Best Local Similarity 99.8%; Pred. No. 3.6e-180;  
 Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MSHGASSRPATARKSSGSLGTVRIPEDKSIHSRSFMEGLASGETRTITLGEEDVYING 60  
 DB 1 MSHGASSRPATARKSSGSLGTVRIPEDKSIHSRSFMEGLASGETRTITLGEEDVYING 60  
 QY 61 KAMQAMGARIRKEGDTWIIDVGNGLAPAPLDFGNATGCRITMGLVGYDFDSTFI 120  
 DB 61 KAMQAMGARIRKEGDTWIIDVGNGLAPAPLDFGNATGCRITMGLVGYDFDSTFI 120  
 QY 121 GDSILTKRPMGVLNPLREMGVQVXSEDDRLPVTLRGKPTPTPIYRVPMASQVKSAY 180  
 DB 121 GDSILTKRPMGVLNPLREMGVQVXSEDDRLPVTLRGKPTPTPIYRVPMASQVKSAY 180  
 QY 181 LLAGINTPGITTVIPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGRKLTGQVID 240  
 DB 181 LLAGINTPGITTVIPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGRKLTGQVID 240  
 QY 241 VPGDPSSTAFPLVAALLVGS DVTILNVLNMPTRTGLITLQEMGADIVINPRLAGSD 300  
 DB 241 VPGDPSSTAFPLVAALLVGS DVTILNVLNMPTRTGLITLQEMGADIVINPRLAGSD 300

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OY 301 VADLRVRSSTLKGVTPEDRAPSMIDEPYITLAVAAAFAGATVMNGLEELRYKESDRLSA 360
DB 301 VADLRVRSSTLKGVTPEDRAPSMIDEPYITLAVAAAFAGATVMNGLEELRYKESDRLSA 360
OY 361 VANGKLKMGVDCDEGETSLVVRGPRDGKGLGNASGAATAVTHLDHRIAMSLVMGLVSENP 420
DB 361 VANGKLKMGVDCDEGETSLVVRGPRDGKGLGNASGAATAVTHLDHRIAMSLVMGLVSENP 420
OY 421 VTVDATMIATSFPEFMDLMAGLGAKIELSDTKAA 455
DB 421 VTVDATMIATSFPEFMDLMAGLGAKIELSDTKAA 455

RESULT 8
AAW24474
ID AAW24474 standard; protein; 455 AA.
AC AAW24474;
XX
XX 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 02-OCT-1997 (first entry)
XX
DE Class II EPSs for glyphosate resistant plant production.
KM 5-enolpyruvylshikimate-3-phosphate synthase; EPSs; Class II;
KM glyphosate resistant; transgenic plant; herbicide; shikimic acid;
KM fusion protein; soybean; corn; wheat; barley; cotton; sugarbeet; tobacco.
OS Agrobacterium sp; strain CP4.
XX
XX US5633435-A.
FN
XX 27-MAY-1997.
PD
XX 13-SEP-1994; 94US-00306063.
PF
XX 31-AUG-1990; 90US-00576537.
PR 28-AUG-1991; 91US-00749611.
XX
XX (MONS ) MONSANTO CO.
PA
PI Padgett SR, Stallings WC, Barry GF, Kishore GM;
XX
XX WPI; 1997-297418/27.
DR N-PSDB; AAT77313.
XX
XX New isolated 5-enol:pyruvyl:shikimate-3-phosphate synthase gene - used
PT for transforming plants to produce plants which are tolerant to
PT glyphosate herbicide.
XX
XX Claim 1; Col 57-60; 154pp; English.
PS
XX AAW24474 shows the sequence of a class II 5-enolpyruvylshikimate-3-
CC phosphate synthase (EPSPS) enzyme. Class II EPSs enzymes are tolerant to
CC glyphosate herbicides. EPSs and sequences encoding it are used for the
CC production of herbicide resistant (glyphosate-tolerant) plants such as
CC corn, wheat, rice, barley, soybean, cotton, sugarbeet, oilseed rape,
CC canola, flax, sunflower, potato, tobacco, tomato, alfalfa, poplar, pine,
CC eucalyptus, apple, lettuce, peas, lentils, grape and turf grasses.
CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 455 AA;
SQ
Query Match 99.7%; Score 2282; DB 2; Length 455;
Best Local Similarity 99.8%; Pred. No. 3.6e-180;
Matches 454; Conservative 0; Mismatch 1; Indels 0; Gaps 0;
OY 1 MLHGASRPATARKSSGSLGTVRIPGDKISHRSFMFGLASGETITGLGSEDTYNTG 60
DB 1 MSHGASRPATARKSSGSLGTVRIPGDKISHRSFMFGLASGETITGLGSEDTYNTG 60

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OY 61 KAMQMGARIRKEGDTWIIDGVNGGLIAPAPLDFGNAATGCRITWGLVGVDYDFSTFI 120
DB 61 KAMQMGARIRKEGDTWIIDGVNGGLIAPAPLDFGNAATGCRITWGLVGVDYDFSTFI 120
OY 121 GDASLTKRPMKRVINPLAEEMGVQVKSIEDGRLPVTLRGPKTPTPTTYVPMASQVKSAY 180
DB 121 GDASLTKRPMKRVINPLAEEMGVQVKSIEDGRLPVTLRGPKTPTPTTYVPMASQVKSAY 180
OY 181 LLAGINTGITTIVLEPIITRDHTEKMLQFGANLIVETDADGVRTIRLEGKGLTGQYID 240
DB 181 LLAGINTGITTIVLEPIITRDHTEKMLQFGANLIVETDADGVRTIRLEGKGLTGQYID 240
OY 241 VPGDPSSTAFPLVAALVPGSDVTITLVNLPRTGLITLTQEMGADIEVINPLAGGED 300
DB 241 VPGDPSSTAFPLVAALVPGSDVTITLVNLPRTGLITLTQEMGADIEVINPLAGGED 300
OY 301 VADLRVRSSTLKGVTPEDRAPSMIDEPYITLAVAAAFAGATVMNGLEELRYKESDRLSA 360
DB 301 VADLRVRSSTLKGVTPEDRAPSMIDEPYITLAVAAAFAGATVMNGLEELRYKESDRLSA 360
OY 361 VANGKLKMGVDCDEGETSLVVRGPRDGKGLGNASGAATAVTHLDHRIAMSLVMGLVSENP 420
DB 361 VANGKLKMGVDCDEGETSLVVRGPRDGKGLGNASGAATAVTHLDHRIAMSLVMGLVSENP 420
OY 421 VTVDATMIATSFPEFMDLMAGLGAKIELSDTKAA 455
DB 421 VTVDATMIATSFPEFMDLMAGLGAKIELSDTKAA 455

RESULT 9
AAW71609
ID AAW71609 standard; protein; 455 AA.
XX
XX AAW71609;
AC
XX 14-DEC-1998 (first entry)
DT
XX
XX Agrobacterium sp. strain CP4 Class II EPSs.
DE
XX
XX 5-enolpyruvylshikimate-3-phosphate synthase; class II EPSs enzyme;
KM glyphosate herbicide; transformed bacteria; class I EPSs enzyme;
KM resistance; inhibition; 5-enolpyruvyl-3-phosphoshikimic acid;
KM N-phosphomethylglycine.
XX
XX Agrobacterium sp.
OS
XX
XX US5804425-A.
FN
XX 08-SEP-1998.
PD
XX 07-APR-1997; 97US-00833485.
PF
XX 31-AUG-1990; 90US-00576537.
PR 28-AUG-1991; 91US-00749611.
PR 13-SEP-1994; 94US-00306063.
XX
XX (MONS ) MONSANTO CO.
PA
PI Stallings WC, Padgett SR, Barry GF, Kishore GM;
XX
XX WPI; 1998-505657/43.
DR N-PSDB; AAV58009.
XX
XX Glyphosate resistant 5-enol:pyruvyl:shikimate-3-phosphate synthase -
PT useful for characterisation of the enzyme to determine inhibition data
PT values.
XX
XX Claim 3; Fig 3; 152pp; English.
PS
XX
XX An isolated 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) has the
CC sequence domains (I), (II), (III) and (IV): -R-XI-H-X2-E- (I), -G-D-K-X3-
CC (II); -S-A-Q-X4-R- (III); and -N-X5-T-R- (IV). Where XI = G, S, T, C, Y,

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CC N, Q, D or E; X2 and X3 = S or T; X4 and X5 = A, R, N, D, C, Q, E, G, H,  
CC I, L, K, M, F, P, S, T, W, Y or V. The EPSPS enzyme, produced by  
CC recombinant methods, can be used in kinetic studies to determine Ki and  
CC Km values of the enzyme for its characterisation. The enzyme is normally  
CC used for the production of 5-enolpyruvyl-3-phosphoshikimate acid in  
CC plants, and most forms of the enzyme are inhibited by N-  
CC phosphonomethylglycine ('glyphosate') herbicides. Inhibition data enables  
CC more accurate values of concentrations of herbicide to be used when  
CC growing the plant without being detrimental to it. This enables the plant  
CC to be grown in the presence of the herbicide, being used to inhibit the  
CC growth of undesired plants. The present sequence represents a Class II  
CC EPSPS from bacterial isolate Agrobacterium sp. strain CP4

Sequence 455 AA;

Query Match 99.7%; Score 2282; DB 2; Length 455;  
Best Local Similarity 99.8%; Pred. No. 3.6e-180;  
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSHGASSRPAATARKSSGSGTIRIPGDKSISHSRPFGLASGERTITGLGSEDVINTG 60  
DB 1 MSHGASSRPAATARKSSGSGTIRIPGDKSISHSRPFGLASGERTITGLGSEDVINTG 60  
QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLPFGNATGCRITMGLVGYDPESTPI 120  
DB 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLPFGNATGCRITMGLVGYDPESTPI 120  
QY 121 GPASLTTRKPMGRVNLPLREMGVQVKSDEGDRLPVTLRGKPTPTPIYRVPMASQVKSAY 180  
DB 121 GPASLTTRKPMGRVNLPLREMGVQVKSDEGDRLPVTLRGKPTPTPIYRVPMASQVKSAY 180  
QY 181 LLAGINTPGITTVIEPIIMTRDTEKMLQGFANLTVETDADGVRTIRLEGKLTGQVID 240  
DB 181 LLAGINTPGITTVIEPIIMTRDTEKMLQGFANLTVETDADGVRTIRLEGKLTGQVID 240  
QY 241 VPGDSSSTAFPLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSD 300  
DB 241 VPGDSSSTAFPLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSD 300  
QY 301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIILAVAAAFAGATVMNGLEELRYKESDRLSA 360  
DB 301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIILAVAAAFAGATVMNGLEELRYKESDRLSA 360  
QY 361 VANGKLKNGVDDDEGTSLVVRGRPDGKLGNAAGAAVATHLDRIAMSFVWGLVSENP 420  
DB 361 VANGKLKNGVDDDEGTSLVVRGRPDGKLGNAAGAAVATHLDRIAMSFVWGLVSENP 420  
QY 421 VTVDATMTATISFPPEFMDLMAIGAKIELSDTKAA 455  
DB 421 VTVDATMTATISFPPEFMDLMAIGAKIELSDTKAA 455

RESULT 10

AAE05053  
ID AAE05053 standard; protein; 455 AA.

AAE05053;

11-SEP-2003 (revised)  
10-SEP-2001 (first entry)  
Agrobacterium sp. strain CP4; class II EPSPS protein.  
5-enolpyruvylshikimate-3-phosphate synthase; EPSPS; glyphosate;  
transformed bacteria; transgenic plant; herbicide.

OS Agrobacterium sp; CP4.  
XX US6248876-B1.  
XX 19-JUN-2001.  
XX 20-AUG-1996; 98US-00137440.

XX 31-AUG-1990; 90US-00576537.  
PR 28-AUG-1991; 91US-00749611.  
PR 13-SEP-1994; 94US-00306063.  
PR 07-APR-1997; 97US-00833485.  
(MONS ) MONSANTO CO.  
Barry GR, Kishore GM, Padgett SR, Stallings WC;  
WPI; 2001-407326/43.  
DR N-PSDB; AAD09754.  
XX DNA probe capable of use in a polymerase chain reaction for identifying  
PT the presence of a target genomic DNA encoding a 5-enolpyruvylshikimate-3-  
PT phosphate synthase (EPSPS) enzyme.

Claim 3; Fig 3; 152pp; English.

The present invention relates to a DNA probe capable of use in a  
CC polymerase chain reaction for identifying the presence of a target  
CC genomic DNA encoding 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS)  
CC enzyme referred to as class II EPSPS enzyme which is tolerant to  
CC glyphosate. EPSPS genes are useful in producing transformed bacteria and  
CC transgenic plants which are tolerant to glyphosate herbicide. The probe  
CC is useful for identifying the presence of a target genomic DNA encoding a  
CC EPSPS enzyme. The present sequence is Agrobacterium sp. strain CP4 class  
CC II EPSPS protein. Note: The present sequence, SBD ID NO: 3 is stated as  
CC amino acid sequence throughout the specification. However, it is referred  
CC as probe in claim 3 of the specification. (Updated on 11-SEP-2003 to  
CC standardise OS field)

Sequence 455 AA;

Query Match 99.7%; Score 2282; DB 4; Length 455;  
Best Local Similarity 99.8%; Pred. No. 3.6e-180;  
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSHGASSRPAATARKSSGSGTIRIPGDKSISHSRPFGLASGERTITGLGSEDVINTG 60  
DB 1 MSHGASSRPAATARKSSGSGTIRIPGDKSISHSRPFGLASGERTITGLGSEDVINTG 60  
QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLPFGNATGCRITMGLVGYDPESTPI 120  
DB 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLPFGNATGCRITMGLVGYDPESTPI 120  
QY 121 GPASLTTRKPMGRVNLPLREMGVQVKSDEGDRLPVTLRGKPTPTPIYRVPMASQVKSAY 180  
DB 121 GPASLTTRKPMGRVNLPLREMGVQVKSDEGDRLPVTLRGKPTPTPIYRVPMASQVKSAY 180  
QY 181 LLAGINTPGITTVIEPIIMTRDTEKMLQGFANLTVETDADGVRTIRLEGKLTGQVID 240  
DB 181 LLAGINTPGITTVIEPIIMTRDTEKMLQGFANLTVETDADGVRTIRLEGKLTGQVID 240  
QY 241 VPGDSSSTAFPLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSD 300  
DB 241 VPGDSSSTAFPLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSD 300  
QY 301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIILAVAAAFAGATVMNGLEELRYKESDRLSA 360  
DB 301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIILAVAAAFAGATVMNGLEELRYKESDRLSA 360  
QY 361 VANGKLKNGVDDDEGTSLVVRGRPDGKLGNAAGAAVATHLDRIAMSFVWGLVSENP 420  
DB 361 VANGKLKNGVDDDEGTSLVVRGRPDGKLGNAAGAAVATHLDRIAMSFVWGLVSENP 420  
QY 421 VTVDATMTATISFPPEFMDLMAIGAKIELSDTKAA 455  
DB 421 VTVDATMTATISFPPEFMDLMAIGAKIELSDTKAA 455

RESULT 11

AAE31621

ID AAE31621 standard; protein; 455 AA.  
 XX AAE31621;  
 AC  
 XX  
 XX  
 DT 24-FEB-2003 (first entry)  
 XX  
 XX  
 DE 5-Enolpyruvylshikimate-3-phosphate synthase (EPSPS).  
 XX  
 XX Agricultural; transgenic; phytopathogenic disease; infection; therapy;  
 KM herbicidal; food process; 5-enolpyruvylshikimate-3-phosphate synthase;  
 KM EPSPS; enzyme.  
 XX  
 XX Unidentified.  
 OS  
 XX WO200284250-A2.  
 XX  
 XX  
 PD 24-OCT-2002.  
 XX  
 XX  
 PF 17-APR-2002; 2002WO-US012014.  
 XX  
 XX  
 PR 17-APR-2001; 2001US-0284273P.  
 PR 18-APR-2001; 2001US-0284713P.  
 XX  
 XX (FEMT-) FEMTOLINK BIOTECHNOLOGIES LLC.  
 PA  
 XX Everett NP, Petell JK, Young SA;  
 PI  
 XX  
 XX WPI; 2003-046937/04.  
 DR  
 XX  
 XX  
 PT Detecting or quantifying target proteins in complex biological samples,  
 PT comprises analyzing peptide fragments via mass spectrometry, where  
 PT detection of a signature peptide indicates the presence of the target  
 PT protein in the sample.  
 PT  
 XX  
 XX Example 3; Fig 3B; 50pp; English.  
 PS  
 XX  
 XX The invention relates to a method for detecting or quantifying target  
 CC proteins in complex biological samples, which involves analyzing peptide  
 CC fragments via mass spectrometry, where detection of a signature peptide  
 CC indicates the presence of the target protein in the sample. The method is  
 CC useful in detecting, quantifying or characterizing target proteins in  
 CC complex biological samples, e.g. plants, animals or microorganisms, by  
 CC employing mass spectrometry-based techniques. It can also be applied in  
 CC agricultural diagnostic analyses, such as detection of genetically  
 CC modified organisms for insect or herbicidal resistance, or in the  
 CC diagnosis of phytopathogenic disease or contamination in plants, soil,  
 CC liquids, solids and other samples from environmental sources. It may also  
 CC be used to monitor for targeted proteins in manufacturing food processes,  
 CC and in various clinical and diagnostic analyses, such as monitoring  
 CC infections and treatment in humans and animals. The present sequence is 5  
 CC -enolpyruvylshikimate-3-phosphate synthase (EPSPS) used to illustrate the  
 CC method of the invention  
 CC  
 XX  
 XX  
 SQ Sequence 455 AA;  
 Query Match 99.7%; Score 2282; DB 6; Length 455;  
 Best Local Similarity 99.8%; Pred. No. 3,6e-180;  
 Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MHGASSRPAATARKSSGSLGVRIIPGDKISHSFMRFGGLASGETITGLBSEEDVING 60  
 DB 1 MHGASSRPAATARKSSGSLGVRIIPGDKISHSFMRFGGLASGETITGLBSEEDVING 60  
 QY 61 KAMQAMGARIRKEGDTWIIDGVNGGILAPAPLDGNAATGRLTMGVGVYDPDSTFI 120  
 DB 61 KAMQAMGARIRKEGDTWIIDGVNGGILAPAPLDGNAATGRLTMGVGVYDPDSTFI 120  
 QY 121 GPASLTFRPMGRVLANPLREMGVOVKSDEGDRPLVTLRGPPTPIYRVPMASQVKSAY 180  
 DB 121 GPASLTFRPMGRVLANPLREMGVOVKSDEGDRPLVTLRGPPTPIYRVPMASQVKSAY 180  
 QY 121 GPASLTFRPMGRVLANPLREMGVOVKSDEGDRPLVTLRGPPTPIYRVPMASQVKSAY 180  
 DB 121 GPASLTFRPMGRVLANPLREMGVOVKSDEGDRPLVTLRGPPTPIYRVPMASQVKSAY 180  
 QY 181 LLAGINTPGITTVIEIMTRDHEKMLQGFGANLTETADAGRTIRLGRGLTGQVID 240  
 DB 181 LLAGINTPGITTVIEIMTRDHEKMLQGFGANLTETADAGRTIRLGRGLTGQVID 240

DB 181 LLAGINTPGITTVIEIMTRDHEKMLQGFGANLTETADAGRTIRLGRGLTGQVID 240  
 QY 241 VPGDSSSTAPFLVAALLVPGSDVTIILNVLNMPRTGILLTLQEMGADIEVINPRLAGGED 300  
 DB 241 VPGDSSSTAPFLVAALLVPGSDVTIILNVLNMPRTGILLTLQEMGADIEVINPRLAGGED 300  
 QY 301 VADLVRSSSTLKGVTPPDRAAPSMIDEYPIILAVAAAFAGATVWNGLEELVYKESDRISA 360  
 DB 301 VADLVRSSSTLKGVTPPDRAAPSMIDEYPIILAVAAAFAGATVWNGLEELVYKESDRISA 360  
 QY 361 VANGKLNGVDCDEGETSLVVRGPRDGKGLGNASGAATVATLDRIRIAMSFLVMGLVSENP 420  
 DB 361 VANGKLNGVDCDEGETSLVVRGPRDGKGLGNASGAATVATLDRIRIAMSFLVMGLVSENP 420  
 QY 421 VTVDATMIATSFPEFMDLMAGLGAKIELSDTKAA 455  
 DB 421 VTVDATMIATSFPEFMDLMAGLGAKIELSDTKAA 455  
 RESULT 12  
 AAE39899  
 ID AAE39899 standard; protein; 455 AA.  
 XX  
 XX  
 AC AAE39899;  
 XX  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 XX  
 DE Agrobacterium sp. strain CP4 class II EPSPS protein.  
 XX  
 XX  
 KM Glyphosate tolerant 5-enolpyruvylshikimate-3-phosphate synthase; enzyme;  
 KM transgenic plant; transgenic; herbicide; weed control; EPSPS.  
 XX  
 XX Agrobacterium sp.  
 XX  
 XX US2002168680-A1.  
 PN  
 XX  
 PD 14-NOV-2002.  
 XX  
 XX  
 PF 16-DEC-1999; 99US-00464099.  
 XX  
 XX  
 PR 31-AUG-1990; 90US-00576537.  
 PR 28-AUG-1991; 91US-00749611.  
 PR 13-SEP-1994; 94US-00306063.  
 PR 07-APR-1997; 97US-00833485.  
 PR 20-AUG-1998; 98US-00137440.  
 XX  
 XX (BARR/) BARRY G F.  
 PA (KISH/) KISHORE G M.  
 PA (PADG/) PADGETTE S R.  
 PA (STAL/) STALLINGS W C.  
 XX  
 XX Barry GF, Kishore GW, Padgette SR, Stallings WC;  
 PI  
 XX  
 DR WPI: 2003-719984/68.  
 DR N-PSDB; AAD60590.  
 XX  
 PT New 5-enolpyruvylshikimate-3-phosphate synthase DNA sequence useful for  
 PT producing genetically transformed plants, and selectively controlling  
 PT weeds in a field containing crop having planted crop seeds or plants.  
 PT  
 XX  
 XX Claim 5; Fig 3; 158pp; English.  
 PS  
 XX  
 XX The invention relates to glyphosate tolerant 5-enolpyruvylshikimate-3-  
 CC phosphate synthase (EPSPS) enzymes and nucleic acid molecules encoding  
 CC such enzymes. The invention is useful for producing genetically  
 CC transformed plants which are tolerant to a glyphosate herbicide and for  
 CC selectively controlling weeds in a field containing a crop having planted  
 CC crop seeds or plants. The present sequence is Agrobacterium sp. strain  
 CC CP4 class II EPSPS protein  
 CC  
 XX  
 SQ Sequence 455 AA;  
 Query Match 99.7%; Score 2282; DB 7; Length 455;  
 QY



Best Local Similarity 99.8%; Pred. No. 3.6e-180;  
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MHGASRRATARKSSGSGTIRIPGDKSISRSFMFGGLASGERITGLGGEVINTG 60
DB 1 MSHGASRRATARKSSGSGTIRIPGDKSISRSFMFGGLASGERITGLGGEVINTG 60
QY 61 KAMQAMGARIKREGDWIIDGVNGGLLAPAPLDPGNATGCRITMGLVGYDPDSTFI 120
DB 61 KAMQAMGARIKREGDWIIDGVNGGLLAPAPLDPGNATGCRITMGLVGYDPDSTFI 120
QY 121 GPASLTKRPMGVNLPLEMGVQVKSDEGDRPLVTLRGKPTPTITTYRVPMASQVKSXV 180
DB 121 GPASLTKRPMGVNLPLEMGVQVKSDEGDRPLVTLRGKPTPTITTYRVPMASQVKSXV 180
QY 181 LLAGANTPGITTVIEPIMTDRDHEKMLQGFANLTVETDADGVRTIRLEGRKLTGOVID 240
DB 181 LLAGANTPGITTVIEPIMTDRDHEKMLQGFANLTVETDADGVRTIRLEGRKLTGOVID 240
QY 241 VEGDPSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLITLQEMGADIEVINPRLAGSD 300
DB 241 VEGDPSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLITLQEMGADIEVINPRLAGSD 300
QY 301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIIAVAAAFAGATVMNGLEELRYKESDRLSA 360
DB 301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIIAVAAAFAGATVMNGLEELRYKESDRLSA 360
QY 361 VANGKLKNGVDCDEGTSLVVRGPRDGKLGNAAGAAVATHLDRHANSFLVMGLVSENP 420
DB 361 VANGKLKNGVDCDEGTSLVVRGPRDGKLGNAAGAAVATHLDRHANSFLVMGLVSENP 420
QY 421 VTVDATMTATSPPEFMDMAGLAKIELSDTKAA 455
DB 421 VTVDATMTATSPPEFMDMAGLAKIELSDTKAA 455

```

## RESULT 13

AAR22301  
ID AAR22301 standard; protein; 449 AA.

AC AAR22301;

XX 24-OCT-2003 (revised)  
DT 03-AUG-1992 (first entry)

XX Class II BPSPS enzyme.

XX Glyphosate tolerant bacteria; herbicides; glyphosate resistant plants;  
KM 5'-enolpyruvylshikimate-3-phosphate synthase; weed control.

OS Achromobacter sp; strain LBNA.

XX WO9204449-A.

XX 19-MAR-1992.

XX 28-AUG-1991; 91WO-US006148.

XX 31-AUG-1990; 90US-00576537.

XX (MONS ) MONSANTO CO.

XX Barry GF, Kishore GM, Padgett SR;

XX WPI; 1992-114356/14.

XX DNA encoding class II 5'-enolpyruvyl shikimate-3-phosphate synthase - for  
PT producing plants and bacteria tolerant to glyphosate herbicides.

XX Disclosure; Fig 5; 148pp; English.

XX The sequence is that of the Class II 5'-enolpyruvylshikimate-3 phosphate  
CC synthase enzyme (BPSPS) of Achromobacter sp. strain LBNA It is used to

CC create glyphosate resistant plants or seeds which can be planted in a  
CC field of crops to selectively control weeds. The crops selected for are  
CC e.g. corn, wheat, rice, oilseed rape, tobacco and alfalfa. This provides  
CC a cost effective, environmentally compatible weed control device. See  
CC also AAR22300 and AAR22302. (Updated on 24-OCT-2003 to standardise OS  
CC field)

XX SQ Sequence 449 AA;

Query Match 83.1%; Score 1900.5; DB 2; Length 449;  
Best Local Similarity 82.9%; Pred. No. 1.4e-148;  
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

```

QY 1 MHGASRRATARKSSGSGTIRIPGDKSISRSFMFGGLASGERITGLGGEVINTG 60
DB 1 MSHGASRRATARKSSGSGTIRIPGDKSISRSFMFGGLASGERITGLGGEVINTG 60
QY 61 KAMQAMGARIKREGDWIIDGVNGGLLAPAPLDPGNATGCRITMGLVGYDPDSTFI 120
DB 61 KAMQAMGARIKREGDWIIDGVNGGLLAPAPLDPGNATGCRITMGLVGYDPDSTFI 120
QY 121 GPASLTKRPMGVNLPLEMGVQVKSDEGDRPLVTLRGKPTPTITTYRVPMASQVKSXV 180
DB 121 GPASLTKRPMGVNLPLEMGVQVKSDEGDRPLVTLRGKPTPTITTYRVPMASQVKSXV 180
QY 181 LLAGANTPGITTVIEPIMTDRDHEKMLQGFANLTVETDADGVRTIRLEGRKLTGOVID 240
DB 181 LLAGANTPGITTVIEPIMTDRDHEKMLQGFANLTVETDADGVRTIRLEGRKLTGOVID 240
QY 241 VEGDPSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLITLQEMGADIEVINPRLAGSD 300
DB 241 VEGDPSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLITLQEMGADIEVINPRLAGSD 300
QY 301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIIAVAAAFAGATVMNGLEELRYKESDRLSA 360
DB 301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIIAVAAAFAGATVMNGLEELRYKESDRLSA 360
QY 361 VANGKLKNGVDCDEGTSLVVRGPRDGKLGNAAGAAVATHLDRHANSFLVMGLVSENP 420
DB 361 VANGKLKNGVDCDEGTSLVVRGPRDGKLGNAAGAAVATHLDRHANSFLVMGLVSENP 420
QY 421 VTVDATMTATSPPEFMDMAGLAKIELS 450
DB 421 VTVDATMTATSPPEFMDMAGLAKIELS 447

```

## RESULT 14

AAR22302  
ID AAR22302 standard; protein; 449 AA.

AC AAR22302;

XX 24-OCT-2003 (revised)  
DT 03-AUG-1992 (first entry)

XX Class II BPSPS enzyme.

XX Glyphosate tolerant bacteria; herbicides; glyphosate resistant plants;  
KM 5'-enolpyruvylshikimate-3-phosphate synthase; weed control.

XX Pseudomonas sp; strain PG2982.

XX WO9204449-A.

XX 19-MAR-1992.

XX 28-AUG-1991; 91WO-US006148.

XX 31-AUG-1990; 90US-00576537.

XX (MONS ) MONSANTO CO.

XX Barry GF, Kishore GM, Padgett SR;



```

Db      121 GDASLSKRPMBGRVNLPLREMGVQVEADGDNRMLTLIGPKTANPITYRVPMASAOVKSAY 180
Qy      181 LLAGINTPGITTVIEPIWTRDHEKMLQGFGANLTVEFDAGVRTIRLEGKLTGQVID 240
Db      181 LLAGINTPGVTVIEPIWTRDHEKMLQGFGANLTVEFDAGVRTIRLEGKLTGQVID 240
Qy      241 VGDPSSTAFPLVALLVPGSDVTILNVMNPTRTGLILLOEMGADIEVINPRLAGSD 300
Db      241 VGDPSSTAFPLVALLVPGSDVTILNVMNPTRTGLILLOEMGADIEVINPRLAGSD 300
Qy      301 VADLRVRSSTLKGVTVPEDRAPSMIDEPILAVAAFAAGATVMNGLEELRVKESDRLSA 360
Db      301 VADLRVRSSTLKGVTVPEDRAPSMIDEPILAVAAFAAGATVMNGLEELRVKESDRLSA 360
Qy      361 VANGKLKNGVDDDEGTSIVRGRPDGKLGNAAGAAVATHDRIAMSFYMGJVSBNP 420
Db      361 VANGKLKNGVDDDEGTSIVRGRPDGKLGNAAGAAVATHDRIAMSFYMGJVSBNP 420
Qy      421 VTVDATMTATSPFEPMDMAGIGAKIELS 450
Db      418 VTVDSDNMATISFPFEPMDMAGIGAKIELS 447

```

Search completed: April 20, 2005, 15:23:13  
 Job time : 78 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Comphen Ltd.

OM protein - protein search, using sw model

Run on: April 20, 2005, 15:19:11 ; Search time 73 Seconds  
(without alignments)  
3191.726 Million cell updates/sec

Title: US-10-622-201-70  
Perfect score: 2288  
Sequence: 1 MLHGASSRPATARKSSGLSG.....FMDLMAIGAKIELSDTKAA 455

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : UniProt 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_crembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2288	100.0	455	2	Q71LY8 glycine max
2	2282	99.7	455	1	Q914E4 agrobacteri
3	2088	91.7	455	1	Q924V5 rhizobium m
4	1900.5	83.1	449	1	P56952 pseudomonas
5	1881.5	82.2	450	1	Q83C44 bruceella su
6	1874.5	81.9	450	1	Q8Y6G1 bruceella me
7	1855.5	81.1	450	1	Q9A9V2 bruceella ab
8	1783	77.9	452	1	Q98C61 rhizobium l
9	1505.5	65.8	442	2	Q6G6X3 bartonella
10	1479.5	64.7	442	2	Q6G545 bartonella
11	1252.5	54.7	445	2	Q6NDP4 rhodospirillum rubrum
12	1228.5	53.7	446	1	Q89WF2 bradyrhizobium
13	1135	49.6	443	1	Q9A2H2 pseudomonas
14	989.5	43.2	746	2	Q9H2G9 pseudomonas
15	970.5	42.4	746	2	Q88K05 pseudomonas
16	942.5	41.2	748	2	Q6FA95 pseudomonas
17	927.5	40.5	454	1	Q87BU2 xylella fae
18	916.5	40.1	438	1	Q8P395 xanthomonas
19	912.5	39.9	454	1	Q9P211 xylella fae
20	904.5	39.5	440	1	Q8P1Y5 xanthomonas
21	889	39.3	429	2	Q749Y6 xanthomonas
22	884	38.6	431	1	Q9KCA6 bacillus th
23	879.5	38.4	429	1	Q8EC11 oceanobacill
24	867.5	37.9	447	1	Q59975 oceanobacill
25	850.5	37.2	440	1	Q8D1Y3 synecococc
26	848	37.1	441	2	Q7U7H8 synecococc
27	842.5	36.8	438	2	Q83E11 coxiella bu
28	840.5	36.7	441	2	Q7V8F4 pseudomonas
29	825	36.1	430	1	Q8K1I9 streptococc
30	824.5	36.0	429	2	Q63A07 bacillus ce
31	824.5	36.0	429	2	Q736A7 bacillus ce

32	823.5	36.0	429	2	Q81C45 bacillus ce
33	822	35.9	427	1	Q8H1F8 streptococc
34	820.5	35.9	429	1	Q6H1F8 bacillus th
35	820	35.8	430	1	Q92483 streptococc
36	817.5	35.7	423	1	Q8R1I1 thermomonas
37	815.5	35.6	428	1	Q92485 listeria in
38	813.5	35.6	427	1	Q84UV8 streptococc
39	813.5	35.6	429	2	Q81P64 bacillus an
40	812	35.5	428	2	Q651J9 bacillus l1
41	807.5	35.3	432	2	Q7NLT3 gloeobacter
42	806.5	35.2	430	1	Q9CEU0 lactococcus
43	806	35.2	443	1	Q9A500 streptococc
44	803.5	35.1	427	1	Q9A500 streptococc
45	802.5	35.1	430	1	P43905 lactococcus

## ALIGNMENTS

RESULT 1	PRELIMINARY	PRT	455 AA.
Q71LY8			
Q71LY8			
AC	Q71LY8		
DT	05-JUL-2004 (TREMBLrel. 27, Created)		
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)		
DE	CP48BSPS.		
OS	Glycine max (soybean).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.		
OX	NCBI_TaxId=3847;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Son D.-Y., Lee S.-I.,		
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.		
CC	-1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =		
CC	phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.		
CC	-1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;		
CC	sixth step.		
CC	-1- SIMILARITY: Belongs to the EPSP synthase family.		
DR	EMBL; AF64188; AAL67577.1; -		
DR	GO; GO:0003866; P:3-phosphoshikimate 1-carboxyvinyltransferase. ; IEA.		
DR	GO; GO:0016740; P:transferase activity; IEA.		
DR	GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . ; IEA.		
DR	InterPro; IPR006264; AroA_Ctransf.		
DR	InterPro; IPR001986; EPSP_synth.		
DR	Pfam; PF00275; EPSP synthase; 1.		
DR	Pfam; PF001667; EPSP synth; 1.		
DR	TIGRfam; TIGR01356; aroA; 1.		
DR	PROSITE; PS00104; EPSP_SYNTHASE_1; 1.		
DR	PROSITE; PS00885; EPSP_SYNTHASE_2; 1.		
KW	Amino-acid biosynthesis; Aromatic amino acid biosynthesis;		
KW	transferase.		
SQ	SEQUENCE 455 AA; 47614 MW; C82D18307E4AD2C3 CRC64;		
Query Match	100.0%; Score 2288; DB 2; Length 455;		
Best Local Similarity	100.0%; Pred. No. 7.8e-129; Indels 0; Gaps 0;		
Matches	455; Conservative 0; Mismatches 0;		
QY	1 MLHGASSRPATARKSSGLSGTIRIPDKISHSRPFMGGLASGETRTGLLGEEDVINTG 60		
DB	1 MLHGASSRPATARKSSGLSGTIRIPDKISHSRPFMGGLASGETRTGLLGEEDVINTG 60		
QY	61 KAMQAMGARIRKEDGTWIIDVGNGLLAPEAPLDGNAATGCRITMGLVGVYDFDSTFI 120		
DB	61 KAMQAMGARIRKEDGTWIIDVGNGLLAPEAPLDGNAATGCRITMGLVGVYDFDSTFI 120		
QY	121 GNASLTKRPMGVNPLREMGVQVSEDDRLPYTLRGKTPPTTYRPMASAOVKSAY 180		
DB	121 GNASLTKRPMGVNPLREMGVQVSEDDRLPYTLRGKTPPTTYRPMASAOVKSAY 180		
QY	181 LLAGINTPGITTVIEIPITRDTKMLQGFGANLTVETDADGVRTIRLEGRKLQGV 240		

```

Db      161 LLAGNTPGITTVIPIMTRDHTKMLQGFANLTVETDADGVRTIRLEGSKLTGQVID
OY      241 VPGDSSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLITLQEMGADIEVINPRLAGGED
Db      241 VPGDSSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLITLQEMGADIEVINPRLAGGED
OY      301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYILAFAAFAEGATVMNGLEELRVKESDRLSA
Db      301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYILAFAAFAEGATVMNGLEELRVKESDRLSA
OY      361 VANGKLNKGVDCDEBETSLVVRGPRDGKGLGNASGAATAVTHLDHRIAMSLVMGLVSENP
Db      361 VANGKLNKGVDCDEBETSLVVRGPRDGKGLGNASGAATAVTHLDHRIAMSLVMGLVSENP
OY      421 VTVDATMIATISFPEFMDLMAGLGAKEIISDTKAA
Db      421 VTVDATMIATISFPEFMDLMAGLGAKEIISDTKAA

```

## RESULT 2

AROQ\_AGRSP STANDARD; PRT; 455 AA.

```

AC      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
GN      enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
OS      Agrobacterium sp. (strain CP4).
OC      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC      Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX      NCBI_TaxID=361;
RN      [1]
RP      SEQUENCE FROM N.A., AND SEQUENCE OF 1-28; 47-61 AND 321-333.
RA      Barry G.F., Kishore G.M., Padgett S.R., Stallings W.C.;
RT      "Glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthases.";
RL      Patent number US5633435, 27-MAY-1997.
RN      [2]
RP      SEQUENCE OF 1-15.
RA      MEDLINE=96182485; PubMed=8598558;
RA      Harrison L.A., Bailey M.R., Naylor M.W., Ream J.E., Hammond B.G.,
RA      Nida D.J., Burnette B.L., Nickson T.E., Milsby T.A., Taylor M.L.,
RA      Fuchs R.L., Padgett S.R.;
RT      "The expressed protein in glyphosate-tolerant soybean, 5-
RT      enolpyruvylshikimate-3-phosphate synthase from Agrobacterium sp.
RT      strain CP4, is rapidly digested in vitro and is not toxic to acutely
RT      gavaged mice.";
RL      J. Nutr. 126:728-740(1996).
CC      -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC      phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC      -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC      sixth step.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC      -1- BIOTECHNOLOGY: Introduced by genetic manipulation and expressed in
CC      glyphosate-tolerant soybean, canola, cotton and maize by Monsanto.
CC      Developed to provide new weed-control options for farmers.
CC      Expression of this protein in plants imparts high levels of
CC      glyphosate tolerance.
CC      -1- SIMILARITY: Belongs to the EPSP synthase family.
DR      HAMMP; MF_00210; -.
DR      InterPro; IPR006264; AroA.
DR      InterPro; IPR001986; EPSP_synth.
DR      Pfam; PF00275; EPSP_synthase; 1.
DR      ProDom; PD00167; EPSP_synth; 1.
DR      TIGRFAMs; TIGR01356; aroA; 1.
DR      PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
DR      PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
KW      Aromatic amino acid biosynthesis; Direct protein sequencing;
KW      Genetically modified food; Herbicide resistance; Transferase.
FT      CONFLICT 2 455 AA; 4758 MW; 236580D08DEP422 CRC64;
SQ      SEQUENCE

```

Query Match 99.7%; Score 2282; DB 1; Length 455;  
 Best Local Similarity 99.8%; Pred. No. 1.8e-128;  
 Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY      1 MLHGASSRPATARKSSGSGVTRIPGDKSISHRSFMFGLASGERIRIGLLEGEDVINTG
Db      1 MSHGASSRPATARKSSGSGVTRIPGDKSISHRSFMFGLASGERIRIGLLEGEDVINTG
OY      61 KAMQAMGARIRKEGDTWIIIDGVNGGLAPAPLPDFGNAATGCRLLTMGLVGYDPDSYFI
Db      61 KAMQAMGARIRKEGDTWIIIDGVNGGLAPAPLPDFGNAATGCRLLTMGLVGYDPDSYFI
OY      121 GDASITKRPKMGVNLPLEMGVQVKSDEGRLPVTLRCPKPTPTTYRVPMASQVKSAY
Db      121 GDASITKRPKMGVNLPLEMGVQVKSDEGRLPVTLRCPKPTPTTYRVPMASQVKSAY
OY      180 121 GDASITKRPKMGVNLPLEMGVQVKSDEGRLPVTLRCPKPTPTTYRVPMASQVKSAY
Db      180 121 GDASITKRPKMGVNLPLEMGVQVKSDEGRLPVTLRCPKPTPTTYRVPMASQVKSAY
OY      240 161 LLAGNTPGITTVIPIMTRDHTKMLQGFANLTVETDADGVRTIRLEGSKLTGQVID
Db      240 161 LLAGNTPGITTVIPIMTRDHTKMLQGFANLTVETDADGVRTIRLEGSKLTGQVID
OY      300 241 VPGDSSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLITLQEMGADIEVINPRLAGGED
Db      300 241 VPGDSSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLITLQEMGADIEVINPRLAGGED
OY      360 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYILAFAAFAEGATVMNGLEELRVKESDRLSA
Db      360 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYILAFAAFAEGATVMNGLEELRVKESDRLSA
OY      420 361 VANGKLNKGVDCDEBETSLVVRGPRDGKGLGNASGAATAVTHLDHRIAMSLVMGLVSENP
Db      420 361 VANGKLNKGVDCDEBETSLVVRGPRDGKGLGNASGAATAVTHLDHRIAMSLVMGLVSENP
OY      455 421 VTVDATMIATISFPEFMDLMAGLGAKEIISDTKAA
Db      455 421 VTVDATMIATISFPEFMDLMAGLGAKEIISDTKAA

```

## RESULT 3

AROQ\_RHIME STANDARD; PRT; 455 AA.

```

AC      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
GN      enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
OS      Name=aroA; OrderedlocusNames=R00253; ORFNames=SMC00333;
OS      Rhizobium meliloti (Sinorhizobium meliloti).
OC      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC      Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX      NCBI_TaxID=382;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      STRAIN=1021;
RA      MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RA      Capela D., Bailey-Hubler F., Couzy J., Bothe G., Ampe F., Batut J.,
RA      Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA      Godt T., Goffeau A., Kahn D., Kiss E., Lelaune V., Masny D.,
RA      Pohl T., Portetelle D., Puehler A., Fumelle B., Ramsperger U.,
RA      Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RT      "Analysis of the chromosome sequence of the legume symbiont
RT      Sinorhizobium meliloti strain 1021.";
RL      Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC      -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC      phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC      -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC      sixth step.
CC      -1- SIMILARITY: Monomer (By similarity).
CC      -1- SUBUNIT: Monomer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC      -1- SIMILARITY: Belongs to the EPSP synthase family.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

DR EMBL: AL591783; CAC41690.1; --  
DR HAMAP: MF 00210; -- 1.  
DR InterPro: IPR006264; AroA.  
DR InterPro: IPR001986; EPSP\_synth.  
DR Pfam: PF00275; EPSP\_synthase; 1.  
DR ProDom: PD001867; EPSP\_synthase; 1.  
DR TIGRFAMs: TIGR01356; aroA; 1.  
DR PROSITE: PS00104; EPSP\_SYNTHASE\_1; 1.  
DR PROSITE: PS00885; EPSP\_SYNTHASE\_2; 1.  
DR Aromatic amino acid biosynthesis; Complete proteome; Transferase.  
SQ SEQUENCE 455 AA; 47900 MW; 97659E1C7B1021B5 CRC64;

Query Match 91.7%; Score 2098; DB 1; Length 455;  
Best Local Similarity 90.5%; Pred. No. 1.8e-117;  
Matches 412; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

QY 1 MLHGSRPATARKSGSLGTVRIPGDKSISRSFMFGGLASGETRITGLGEGDVINTG 60  
DB 1 MSHGSNPRATARKSDDLKGTLRIPGDKSISRSFMFGGLASGETRITGLGEGDVINTG 60  
QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLDFGNATGCRITMGLVGYDPTSTI 120  
DB 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLDFGNATGCRITMGLVGYDPTSTI 120  
QY 121 GPASLTGRMGVNLPLREMGVOVKSBDRLPVTLRGKPTPTPIYRVPMAAQVKSXAV 180  
DB 121 GPASLTGRMGVNLPLREMGVOVKSBDRLPVTLRGKPTPTPIYRVPMAAQVKSXAV 180  
QY 181 LLAGINTPGITTVIEPIIMRDTHEKMLQGFGANLVETDADGRTIRLEGRGLTGQVID 240  
DB 181 LLAGINTPGITTVIEPIIMRDTHEKMLQGFGANLVETDADGRTIRLEGRGLTGQVID 240  
QY 241 VEGDPSSTAFPLVALLVPGSDVTITLVNMPRTGLITLQEMGADIVINPRLAGSD 300  
DB 241 VEGDPSSTAFPLVALLVPGSDVTITLVNMPRTGLITLQEMGADIVINPRLAGSD 300  
QY 301 VADLRVRSSTLKGTVPEDRAPSMIDEPYTLVAAAFAGATVMNGLEELRYKESDRLA 360  
DB 301 VADLRVRSSTLKGTVPEDRAPSMIDEPYTLVAAAFAGATVMNGLEELRYKESDRLA 360  
QY 361 VANGKLKLVGDDCEGTSLVVGRPDGKLGNAAGAAVTHLDHRTAMSFVWGLVSENP 420  
DB 361 VADGLKLVGDDCEGASLVVGRPDGKLGKISGQGVTHLDHRTAMSFVWGLVSENP 420  
QY 421 VTVDATMTATSPFERMDLMAIGAKIELSDTYAA 455  
DB 421 VTVDATMTATSPFERMDLMAIGAKIELSDTYAA 455

RESULT 4  
AROA\_PSES2  
ID AROA\_PSES2 STANDARD; PRT; 449 AA.  
AC P56952;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-  
enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPs).  
GN Name=aroA;  
OS Pseudomonas sp. (strain PG2982), and  
OS Acetomobacter sp. (strain LBAA).  
OC Bacteria; Proteobacteria.  
OX NCBI\_TaxID=308, 129026;  
RN (1)  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 2-16.  
RA Barry G.F., Kishore G.M., Padgett S.R., Stallings W.C.;

RT "Glyphosate-tolerant 5-enolpyruvylshikimate-3-phosphate synthases."  
RL Patent number US633435, 27-MAY-1997.  
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =  
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.  
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;  
CC sixth step.

CC -1- SUBUNIT: Monomer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
CC -1- MISCELLANEOUS: Resistant to the antibiotic glyphosate.  
CC -1- SIMILARITY: Belongs to the EPSP synthase family.  
DR HAMAP: MF 00210; -- 1.  
DR InterPro: IPR006264; AroA.  
DR InterPro: IPR001986; EPSP\_synth.  
DR Pfam: PF00275; EPSP\_synthase; 1.  
DR ProDom: PD001867; EPSP\_synthase; 1.  
DR TIGRFAMs: TIGR01356; aroA; 1.  
DR PROSITE: PS00104; EPSP\_SYNTHASE\_1; 1.  
DR PROSITE: PS00885; EPSP\_SYNTHASE\_2; 1.  
DR Aromatic amino acid biosynthesis; Direct protein sequencing;  
KW Herdicide resistance; Transferase.  
SQ SEQUENCE 449 AA; 47297 MW; 447F213EECCAEFC1 CRC64;

Query Match 83.1%; Score 1900.5; DB 1; Length 449;  
Best Local Similarity 82.9%; Pred. No. 1.1e-105;  
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

QY 1 MLHGSRPATARKSGSLGTVRIPGDKSISRSFMFGGLASGETRITGLGEGDVINTG 60  
DB 1 MSHGSNPRATARKSDDLKGTLRIPGDKSISRSFMFGGLASGETRITGLGEGDVINTG 60  
QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLDFGNATGCRITMGLVGYDPTSTI 120  
DB 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLDFGNATGCRITMGLVGYDPTSTI 120  
QY 121 GPASLTGRMGVNLPLREMGVOVKSBDRLPVTLRGKPTPTPIYRVPMAAQVKSXAV 180  
DB 121 GPASLTGRMGVNLPLREMGVOVKSBDRLPVTLRGKPTPTPIYRVPMAAQVKSXAV 180  
QY 181 LLAGINTPGITTVIEPIIMRDTHEKMLQGFGANLVETDADGRTIRLEGRGLTGQVID 240  
DB 181 LLAGINTPGITTVIEPIIMRDTHEKMLQGFGANLVETDADGRTIRLEGRGLTGQVID 240  
QY 241 VEGDPSSTAFPLVALLVPGSDVTITLVNMPRTGLITLQEMGADIVINPRLAGSD 300  
DB 241 VEGDPSSTAFPLVALLVPGSDVTITLVNMPRTGLITLQEMGADIVINPRLAGSD 300  
QY 301 VADLRVRSSTLKGTVPEDRAPSMIDEPYTLVAAAFAGATVMNGLEELRYKESDRLA 360  
DB 301 VADLRVRSSTLKGTVPEDRAPSMIDEPYTLVAAAFAGATVMNGLEELRYKESDRLA 360  
QY 361 VANGKLKLVGDDCEGTSLVVGRPDGKLGNAAGAAVTHLDHRTAMSFVWGLVSENP 420  
DB 361 VADGLKLVGDDCEGASLVVGRPDGKLGKISGQGVTHLDHRTAMSFVWGLVSENP 420  
QY 421 VTVDATMTATSPFERMDLMAIGAKIELSDTYAA 450  
DB 421 VTVDATMTATSPFERMDLMAIGAKIELSDTYAA 450

RESULT 5  
AROA\_BRUSU  
ID AROA\_BRUSU STANDARD; PRT; 450 AA.  
AC O86374;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-  
enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPs).  
GN Name=aroA; Ordered locus Names=BR0025;  
OS Brucella suis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Brucellaceae; Brucella.  
OX NCBI\_TaxID=29461;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biotype 1;
RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J.A.,
RA Van Aken S.E., Riedmiller S., Tettelin H., Gill S.R., White O.,
RA Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
RA Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13146-13153 (2002).
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
CC -----
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CC -----
DR EMBL; AE014317; AAN28982.1; -
DR TIGR; BR0025; -
DR HAMAP; MF_00210; -; 1.
DR InterPro; IPR006264; AroA.
DR InterPro; IPR001986; EPSP synth.
DR Pfam; PF00275; EPSP synthase; 1.
DR ProDom; PD001867; EPSP_synth; 1.
DR TIGRFAMs; TIGR01356; aroA; 1.
DR PROSITE; PS00104; EPSP SYNTHASE 1; 1.
DR PROSITE; PS00885; EPSP SYNTHASE 2; 1.
DR Aromatic amino acid biosynthesis; Complete proteome; Transferase.
SQ SEQUENCE 450 AA; 47249 MW; E571FAB83C049PDC CRC64;

Query Match 82.2%; Score 1861.5; DB 1; Length 450;
Best Local Similarity 82.1%; Pred. No. 1.5e-104;
Matches 369; Conservative 33; Mismatches 42; Indels 3; Gaps 1;

QY 1 MHGASSRPATARKSGSGTVRIPEGDKSISHSRSMFGGLASGERTITGLLEGEDVINTG 60
DB 1 MSHSACPRTARHQSALTGEIRIPEDKSIHSRSMFGGLASGKTRITGLLEGEDVINTG 60
QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLLAPAPLDFGNATGCRITMGLVGVYDFDSTPI 120
DB 61 RAMQAMGARIRKEGDTWIIDGVNGGLLAPAPLDFGNATGCRITMGLVGVYDFDSTPI 120
QY 121 GPASLTGRPMGVNLPRLRMGVQVKSSEDGRLPVTLRGKPTPIPTIYRVPMASQVKSAY 180
DB 121 GPASLTGRPMGVNLPRLRMGVQVKSSEDGRLPVTLRGKPTPIPTIYRVPMASQVKSAY 180
QY 121 GPASLTGRPMGVNLPRLRMGVQVKSSEDGRLPVTLRGKPTPIPTIYRVPMASQVKSAY 180
DB 121 GPASLTGRPMGVNLPRLRMGVQVKSSEDGRLPVTLRGKPTPIPTIYRVPMASQVKSAY 180
QY 181 LLAGINTPGITVIYRIMRDTHEKMLQSGFANLTIVETDADGVRTRLEGGRGLTGQVID 240
DB 181 LLAGINTPGITVIYRIMRDTHEKMLQSGFADLVETKDXDGRHRIVGQGLTGQVID 240
QY 241 VPGDPSSTAFPLVAALLVPGSDVTILNVAMNPTRTGLITLQEMGADIVINPRLAGSD 300
DB 241 VPGDPSSTAFPLVAALLVPGSDVTIRNVAMNPTRTGLITLQEMGADIIITDRLAGSD 300
QY 301 VADLRVRSSTLKVTVYEDRPASMDIYPIILAVAAAFAGATVWNGLEELRYVESDRLSA 360
DB 301 VADLRVRSSTLKVTVYEDRPASMDIYPIILAVAAAFAGATVWNGLEELRYVESDRLSA 360
QY 361 VADLRVRSSTLKVTVYEDRPASMDIYPIILAVAAAFAGATVWNGLEELRYVESDRLSA 360
DB 361 VADLRVRSSTLKVTVYEDRPASMDIYPIILAVAAAFAGATVWNGLEELRYVESDRLSA 360
QY 361 VANGUKLNVDDDEGTSILVGRPRGKGLGNAAGAAVATHLDHRIAMFLVWGLVSENP 420
DB 361 VANGUKLNVDDDEGTSILVGRPRGKGLGNAAGAAVATHLDHRIAMFLVWGLVSENP 420

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DB 361 VARGLEANGVDCITSEMSLTVRGPRGKGLG---CGTATVTHLDHRIAMFLVWGLASEKP 417
QY 421 VTVDATMIATSPFPEFMDLMAGLAKI 447
DB 418 VTVDSTMIATSPFPEFMDLMAGLAKI 444

RESULT 6
ACROA BRUME STANDARD; PRT; 450 AA.
ID ACROA BRUME
AC 08YEG1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
DE enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
GN Name=aroA; Ordered locus names=BWE11917;
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX PubMed=11756688; DOI=10.1073/pnas.221575398;
RA Delvecchio V.G., Kapetral V., Redkar R.D., Patra G., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonov E., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elser P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyriides N.C., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
CC -----
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CC -----
DR EMBL; AE009625; AAL53098.1; ALT_INIT.
DR HAMAP; MF_00210; -; 1.
DR InterPro; IPR006264; AroA.
DR InterPro; IPR001986; EPSP synth.
DR Pfam; PF00275; EPSP synthase; 1.
DR ProDom; PD001867; EPSP_synth; 1.
DR TIGRFAMs; TIGR01356; aroA; 1.
DR PROSITE; PS00104; EPSP SYNTHASE 1; 1.
DR PROSITE; PS00885; EPSP SYNTHASE 2; 1.
DR Aromatic amino acid biosynthesis; Complete proteome; Transferase.
SQ SEQUENCE 450 AA; 47207 MW; 931C4B483C162CB7 CRC64;

Query Match 81.9%; Score 1874.5; DB 1; Length 450;
Best Local Similarity 82.1%; Pred. No. 4e-104;
Matches 367; Conservative 34; Mismatches 43; Indels 3; Gaps 1;

QY 1 MHGASSRPATARKSGSGTVRIPEGDKSISHSRSMFGGLASGERTITGLLEGEDVINTG 60
DB 1 MSHSACPRTARHQSALTGEIRIPEDKSIHSRSMFGGLASGKTRITGLLEGEDVINTG 60
QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLLAPAPLDFGNATGCRITMGLVGVYDFDSTPI 120
DB 61 RAMQAMGARIRKEGDTWIIDGVNGGLLAPAPLDFGNATGCRITMGLVGVYDFDSTPI 120
QY 121 GPASLTGRPMGVNLPRLRMGVQVKSSEDGRLPVTLRGKPTPIPTIYRVPMASQVKSAY 180
DB 121 GPASLTGRPMGVNLPRLRMGVQVKSSEDGRLPVTLRGKPTPIPTIYRVPMASQVKSAY 180
QY 121 GPASLTGRPMGVNLPRLRMGVQVKSSEDGRLPVTLRGKPTPIPTIYRVPMASQVKSAY 180
DB 121 GPASLTGRPMGVNLPRLRMGVQVKSSEDGRLPVTLRGKPTPIPTIYRVPMASQVKSAY 180
QY 181 LLAGINTPGITVIYRIMRDTHEKMLQSGFANLTIVETDADGVRTRLEGGRGLTGQVID 240
DB 181 LLAGINTPGITVIYRIMRDTHEKMLQSGFADLVETKDXDGRHRIVGQGLTGQVID 240
QY 241 VPGDPSSTAFPLVAALLVPGSDVTILNVAMNPTRTGLITLQEMGADIVINPRLAGSD 300
DB 241 VPGDPSSTAFPLVAALLVPGSDVTIRNVAMNPTRTGLITLQEMGADIIITDRLAGSD 300
QY 301 VADLRVRSSTLKVTVYEDRPASMDIYPIILAVAAAFAGATVWNGLEELRYVESDRLSA 360
DB 301 VADLRVRSSTLKVTVYEDRPASMDIYPIILAVAAAFAGATVWNGLEELRYVESDRLSA 360
QY 361 VADLRVRSSTLKVTVYEDRPASMDIYPIILAVAAAFAGATVWNGLEELRYVESDRLSA 360
DB 361 VADLRVRSSTLKVTVYEDRPASMDIYPIILAVAAAFAGATVWNGLEELRYVESDRLSA 360
QY 361 VANGUKLNVDDDEGTSILVGRPRGKGLGNAAGAAVATHLDHRIAMFLVWGLVSENP 420
DB 361 VANGUKLNVDDDEGTSILVGRPRGKGLGNAAGAAVATHLDHRIAMFLVWGLVSENP 420

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QY 121 GDA$LTRPMGRLNPLREMGVQVKS$EDDRPLVTLRGPKTPPTITRYRPMASQVKSAY 180
DB 121 GDA$SKRPMGRVNLPLREMGVQV$EA$EDDRPLVTLRGPKTPPTITRYRPMASQVKSAY 180
QY 181 LLAGNTPGITTVIEPIWTRDHEKMLQGPGANLVTETDADGVRTIRL$RGKLTQOVID 240
DB 181 LLAGNTPGITTVIEPIWTRDHEKMLQGPGANLVTETDADGVRTIRIVGQGLTQOTID 240
QY 241 VEGDE$STAFPLVALLVPGSDVTINLVNMPRTGLITLQEMGADIEVINPRLAGSD 300
DB 241 VEGDE$STAFPLVALLVPGSDVTINLVNMPRTGLITLQEMGADIEIDPRLAGSD 300
QY 301 VADLRVRS$TLKGVTVPEDRAP$MIDEPYLLAVAA$FAGATVMNGL$EELRVESDRL$A 360
DB 301 VADLRVRS$TLKGVTVPEDRAP$MIDEPYLLAVAA$FAGATVMNGL$EELRVESDRL$A 360
QY 361 VANGKLNGVDCDEGSTLVNRPDPKGLGNASGA$VAATHDRIAMSFLVNGLVSENP 420
DB 361 VANGKLNGVDCDEGSTLVNRPDPKGLGNASGA$VAATHDRIAMSFLVNGLVSENP 420
QY 421 VTVDDATMTATSPF$PFMDLMA$GLGAKI 447
DB 418 VTVDDSTMTATSPF$PFMDLMA$GLGAKI 444

RESULT 7
ARO$ BRUB
ID ARO$ BRUB STANDARD; PRT; 450 AA.
AC 09AGV2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 3-phosphoenolpyruvate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
GN Name=aroA;
OS Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bruciellaceae; Brucella.
OX NCBI_TaxId=235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2308;
RA Gan T., Essenberg R.C.;
RT "Characterization of the aroA gene of Brucella abortus and
construction of an aroA mutant.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
sixth step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
-----
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or send an email to license@isb-sib.ch).
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CC EMBL: AF326475; AKK27445.1; ALT_INT.
DR HAMAP; MF_00210; -; 1.
DR InterPro; IPR006264; AroA.
DR InterPro; IPR001966; EPSP synth.
DR Pfam; PF00275; EPSP synthase; 1.
DR ProDom; PD001867; EPSP synth; 1.
DR TIGRfam; TIGR01356; aroA; 1.
DR PROSITE; PS00104; EPSP SYNTHASE_1; 1.
DR PROSITE; PS00885; EPSP SYNTHASE_2; 1.
KW Aromatic amino acid biosynthesis; Transferase.
SQ SEQUENCE 450 AA; 47264 MW; 371B9F97B2ED9DA4 CRC64;

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Query Match 81.1%; Score 1855.5; DB 1; Length 450;
Best Local Similarity 81.4%; Pred. No. 5,5e-103;
Matches 364; Conservative 35; Mismatches 45; Indels 3; Gaps 1;

QY 1 MHHGASRPATARKSSGLSGTVRIPGDKSISHSFNFGLASGETITGL$EEDVINTG 60
DB 1 MSHSACPKPATRHSQALTEIGRIPGDKSISHSFNFGLASGETITGL$EEDVINTG 60
QY 61 KAMQAMGARIRKRGDPMWIIDGVNGGLAP$EAPL$DGNATGCRITMGLVGVDPSTFI 120
DB 61 RAMQAMGARIRKRGDPMWIIDGVNGGLAP$EAPL$DGNATGCRITMGLVGVDPSTFI 120
QY 121 GDA$LTRPMGRLNPLREMGVQVKS$EDDRPLVTLRGPKTPPTITRYRPMASQVKSAY 180
DB 121 GDA$SKRPMGRVNLPLREMGVQV$EA$EDDRPLVTLRGPKTPPTITRYRPMASQVKSAY 180
QY 181 LLAGNTPGITTVIEPIWTRDHEKMLQGPGANLVTETDADGVRTIRL$RGKLTQOVID 240
DB 181 LLAGNTPGITTVIEPIWTRDHEKMLQGPGANLVTETDADGVRTIRIVGQGLTQOTID 240
QY 241 VEGDE$STAFPLVALLVPGSDVTINLVNMPRTGLITLQEMGADIEVINPRLAGSD 300
DB 241 VEGDE$STAFPLVALLVPGSDVTINLVNMPRTGLITLQEMGADIEIDPRLAGSD 300
QY 301 VADLRVRS$TLKGVTVPEDRAP$MIDEPYLLAVAA$FAGATVMNGL$EELRVESDRL$A 360
DB 301 VADLRVRS$TLKGVTVPEDRAP$MIDEPYLLAVAA$FAGATVMNGL$EELRVESDRL$A 360
QY 361 VANGKLNGVDCDEGSTLVNRPDPKGLGNASGA$VAATHDRIAMSFLVNGLVSENP 420
DB 361 VANGKLNGVDCDEGSTLVNRPDPKGLGNASGA$VAATHDRIAMSFLVNGLVSENP 420
QY 421 VTVDDATMTATSPF$PFMDLMA$GLGAKI 447
DB 418 VTVDDSTMTATSPF$PFMDLMA$GLGAKI 444

RESULT 8
ARO$ RHIL0
ID ARO$ RHIL0 STANDARD; PRT; 452 AA.
AC 098CC1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 3-phosphoenolpyruvate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
GN Name=aroA; Ordered locus Names=ml15213;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OX NCBI_TaxId=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFE30309;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Watanabe A., Ideesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takenuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
RL DNA Res. 7:331-338 (2000).
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
sixth step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the EPSP synthase family.
-----
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CC -----  
 DR EMBL, AP003006; BAB51700.1; --  
 DR HAMAP, MF\_00210; -- 1.  
 DR InterPro; IPR006264; AroA.  
 DR InterPro; IPR001986; Epsp synth.  
 DR Pfam; PF00275; Epsp synthase; 1.  
 DR Prodom; PPO01867; Epsp synth; 1.  
 DR TIGRfam; TIGR01356; aroA; 1.  
 DR PROSITE; PS00104; Epsp SYNTHASE 1; 1.  
 DR PROSITE; PS00885; Epsp SYNTHASE 2; 1.  
 DR Aromatic amino acid biosynthesis; Complete proteome; Transferrase.  
 KW Aromatic amino acid biosynthesis; Complete proteome; Transferrase.  
 SQ SEQUENCE 452 AA; 47455 MW; 2B59383E3523B938 CRC64;

Query Match 77.9%; Score 1783; DB 1; Length 452;  
 Best Local Similarity 77.8%; Pred. No. 1.2e-98;  
 Matches 351; Conservative 33; Mismatches 63; Indels 4; Gaps 2;

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QY 1 MHGASRPATARKSGSLGTVRIGDQKSIHRSFMEGLASGETRTITGLGEDVINTG 60
DB 1 MSHAAAKAPATRKSOALSGLTARVPEDKSISHRSFMEGLASGETRTITGLGEDVINTG 60
QY 61 KAMQAMGARIRKEGDTWIIDVNGGGLAPEAPLDFGNATGRLTMGLVGVDPSTFPI 120
DB 61 AAMKAMGAHIEKGAEMVIRGTNGALLQPEGLDFGNAGTSLRMGLVGVYDMETTFPI 120
QY 121 GDASTITKPMGVNLPLREMGVQV-KSEIDGRLEVTLRGPKTPPTTYRPMASQVSKA 179
DB 121 GPASISGRMGVNLPLREMGVQV-KATPGDMPTITLHGPKAAPITTYRPMASQVSKA 180
QY 180 VLLAGLNTPTGTTVLEPIRTDTEKMLQGFANLTVETDADGVRTIRLEGGKLTGVYI 239
DB 181 VLLAGLNTPTGTTVLEPIRTDTEKMLQGFANLTVETDADGVRTIRLEGGKLTGVYI 240
QY 240 DVPGPSSTAPFLVALALVPGSDVTILNVLNMPTRTGLITLQMGADIEVINPLRAGE 299
DB 241 AVGPSSAGFLVALALVPGSDITENVLNMPTRTGLITLQMGADIEVINPLRAGE 300
QY 300 DVADIRVSSITKGVTPEDRAPSMIDEPYIILAAVAAAFAGATWNGLEELRYKESDRIS 359
DB 301 DVADIRVSSITKGVTPEDRAPSMIDEPYIILAAVAAAFAGATWNGLEELRYKESDRIS 360
QY 360 AVANGKLINGVDCDEGETSLVVRGPRDGKLG--NAGAAVATHLDRILAMSLVWGLV 416
DB 361 AVANGKLINGVDCDEGETSLVVRGPRDGKLG--NAGAAVATHLDRILAMSLVWGLV 420
QY 417 SENPVTDATMTATSPFEMDLMAIGAKI 447
DB 421 TEKPVITIDQAMTATSPFEMDLMAIGAKI 451

```

RESULT 9

06G0X3 PRELIMINARY; PRT; 442 AA.  
 AC 06G0X3;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE 3-phosphoshikimate 1-carboxyvinyltransferase.  
 GN Name=aroA; Ordered locus Names=B000880;  
 OS Bartonella quintana (Rochalimaea quintana).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bartonellaceae; Bartonella.  
 NCBI\_TaxID=803;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Noniouse;  
 PX Pubmed=15210978; DOI=10.1073/pnas.030659101;

RA Almark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,  
 RA Camdeack B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvel M.,  
 RA La Scola B., Holmberg M., Andersson S.G.E.;  
 RT "The louse-borne human pathogen Bartonella quintana is a genomic  
 RT derivative of the zoonotic agent Bartonella henselae.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).  
 CC -1- CARBAMYLIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =  
 CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.  
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;  
 CC sixth step.  
 CC -1- SIMILARITY: Belongs to the Epsp synthase family.  
 DR EMBL; BX897700; CAP25595.1; --  
 DR GO; GO:0003866; P-3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.  
 DR GO; GO:0016740; E:transferase activity; IEA.  
 DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . .; IEA.  
 DR InterPro; IPR006264; AroA Ctransf.  
 DR InterPro; IPR001986; Epsp synth.  
 DR Pfam; PF00275; Epsp synthase; 1.  
 DR Prodom; PPO01867; Epsp synth; 1.  
 DR TIGRfam; TIGR01356; aroA; 1.  
 DR PROSITE; PS00104; Epsp SYNTHASE 1; 1.  
 KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;  
 KW Complete proteome; Transferrase.  
 SQ SEQUENCE 442 AA; 47538 MW; 225F15BCFDF6DBA CRC64;

Query Match 65.8%; Score 1505.5; DB 2; Length 442;  
 Best Local Similarity 68.1%; Pred. No. 4.5e-82;  
 Matches 299; Conservative 51; Mismatches 86; Indels 3; Gaps 1;

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QY 9 PATARKSGSLGTVAIPDQKSIHRSFMEGLASGETRTITGLBEDVINTGKAMQANGA 68
DB 6 PTTAKSITCLSGSLTIPDQKSIHRSITLGGIANSETHHGLBEDVINTGKAMQANGA 65
QY 69 RIRKEGDTWIIDVNGGGLAPEAPLDFGNATGRLTMGLVGVDPSTFPGDASLTRK 128
DB 66 CIKKADMIIRGTNGGGLAERKYNFGNAGTGARLVMGWVGRPHMKTTFIGDASLSR 125
QY 129 PMGRVNLPLREMGVQVKEDEGRLEVTLRGPKTPPTTYRPMASQVSKAVLGLNTP 188
DB 126 PMGRILNPLRLMGVIEATHGDRPLTLTGPDMANPIRYRIPASQVSKATILGLNTP 185
QY 189 GTTYIETPTMRDHEKMLQGFANLTVETDADGVRTIRLEGGKLTGVYIIPGPSST 248
DB 186 GTTYIETPTMRDHEKMLQGFANLTVETDADGVRTIRLEGGKLTGVYIIPGPSST 245
QY 249 AFLVALALVPGSDVTILNVLNMPTRTGLITLQMGADIEVINPLRAGEVDADIRYS 308
DB 246 AFLPIALVENSDDITENVLNMPTRTGLITLQMGADIEVINPLRAGEVDADIRYS 305
QY 309 STLKGVTPEDRAPSMIDEPYIILAAVAAAFAGATWNGLEELRYKESDRISAVANGKLN 368
DB 306 SMLKGVTPEDRAPSMIDEPYIILAAVAAAFAGATWNGLEELRYKESDRISAVANGKLN 365
QY 369 GVDCEGETSLVVRGPRDGKLG--NAGAAVATHLDRILAMSLVWGLVSENVPVTDATM 428
DB 366 HVDCEGETSLVVRGPRDGKLG--NAGAAVATHLDRILAMSLVWGLVSENVPVTDATM 422
QY 429 IATSPFEMDLMAIGAKI 447
DB 423 IATSPFEMDLMAIGAKI 441

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RESULT 10

06G545 PRELIMINARY; PRT; 442 AA.  
 AC 06G545;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE 3-phosphoshikimate 1-carboxyvinyltransferase.  
 GN Name=aroA; Ordered locus Names=BH00950;  
 OS Bartonella henselae (Rochalimaea henselae).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Bartonellaceae; Bartonella.  
 RN NCB1\_Taxid=38323;  
 RP STRAIN=ATCC 49882 / Houston 1;  
 RX PubMed=15210978; DOI=10.1073/pnas.0305659101;  
 RA Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,  
 RA Canaack B., Eriksson A.-S., Naesslund A.K., Handley S.A., Huvel M.,  
 RA La Scala B., Holmberg M., Andersson S.G.E.;  
 RT "The louse-borne human pathogen Bartonella quintana is a genomic  
 RT derivative of the zoonotic agent Bartonella henselae";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101.9716-9721(2004)  
 CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =  
 CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.  
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;  
 CC sixth step.  
 CC -1- SIMILARITY: Belongs to the EPSP synthase family.  
 DR EMBL; BX897699; CAF26911.1; -  
 DR GO; GO:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . .; IEA.  
 DR InterPro; IPR006264; AroC Ctransf.  
 DR InterPro; IPR001986; EPSP\_synth.  
 DR Pfam; PF00275; EPSP\_synthase; 1.  
 DR ProDom; PD001867; EPSP\_synth; 1.  
 DR TIGRFAMs; TIGR01356; aroA; 1.  
 DR PROSITE; PS00104; EPSP SYNTHASE 1; 1.  
 KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;  
 KW Complete proteome; Transferase.  
 SQ SEQUENCE 442 AA; 47515 MW; 1B9D1F951BE1982D CRC64;

Query Match 64.7%; Score 1479.5; DB 2; Length 442;  
 Best Local Similarity 67.0%; Pred. No. 1.6e-80;  
 Matches 294; Conservative 52; Mismatches 90; Indels 3; Gaps 1;  
 QY 9 PATARKSSGLSGTVAIPGDKSISHRSFMFGLASGETRTITGLLEGEDVINTGKAMQAMGA 68  
 DB 6 PMTAVKSTRLSGIKIPGDKSISHRSLIIGLASGETHTHIGLIESDVENTAAMQALGA 65  
 QY 69 RIRKESGDTHIIDGVNGGLAPAPLDFGNATGCLTMGLGVVYDPDSTPIGDASLTR 128  
 DB 66 CIKKODLWIIRGTGNGCLLAQKPLDFGNAGALVGMGVPMKTTPIGDASLSR 125  
 QY 129 PGRVRLNPLREMGVQKSEEDGRLPYTLRGPKTPTITRVPMASQAVKSAVLLAGLNP 188  
 DB 126 PPARILIDPLQMGVEIEATHGNVLPILTYGPKNTNICYRIPASQVKSAILLAGLNTA 185  
 QY 189 GTTIVIEPIMTDRHTEKMLQGFANLTVETDADGVRTIRLEGKSLTGVVIDVPGDPSS 248  
 DB 186 GTTIVIEPILTDRHTEKMLKAFGAKLEIKNAAGTRFIHLNGHPLTGTIHPGDPSSA 245  
 QY 249 APPVLAALLVPGSDVTILNVLNMPRTGILITLQEMGADIEVINPRLAGGEDVADLRVNS 308  
 DB 246 APPVLAALLIEESDITIEVNLINNSRMGIETLMEWGAQIELINQRTGGEDEVANIRVNS 305  
 QY 309 STLKGTVVEDRAPSIMIDEYPILAVAAPFAEGATVWNGJLEELVKSSDRLSAVANGKLN 368  
 DB 306 STLKGTVVEKRAPSIMIDEYPILAVAAPFAEGATVWNGJLEELVKSSDRLSAVANGKLN 365  
 QY 369 GVDCEGETSLVVRGRPDGKLGASGAAVATHLDRILMSFLVWGLVSENPVTVDATM 428  
 DB 366 HYDCEGQDFLIHVGSAKGLG---GVVTHLDRILMSFLIFGLVSEKPTITIDKGM 422  
 QY 429 IATSPFEMDLNAGLAKI 447  
 DB 423 IATSPFEPFIPIQLGSKI 441

RESULT 11  
 Q6NDP4 PRELIMINARY; PRT; 445 AA.  
 AC Q6NDP4;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19).  
 GN Name=aroA; OrderedLocNames=RPA0061;  
 OS Rhodopseudomonas palustris.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae; Rhodopseudomonas.  
 RN NCB1\_Taxid=1076;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CGA009 / ATCC BAA-98;  
 RX PubMed=14704707; DOI=10.1038/nbt923;  
 RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,  
 RA Land M.U., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,  
 RA Gibson J.L., Hanson T.E., Bobst C., Torres Y Torres J.L., Peres C.,  
 RA Harrison F.H., Gibson J., Harwood C.S.;  
 RT "Complete genome sequence of the metabolically versatile  
 RT photosynthetic bacterium Rhodopseudomonas palustris".  
 RL Nat. Biotechnol. 22:55-61(2004).  
 CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =  
 CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.  
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;  
 CC sixth step.  
 CC -1- SIMILARITY: Belongs to the EPSP synthase family.  
 DR EMBL; BX572593; CAE2505.1; -  
 DR GO; GO:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . .; IEA.  
 DR InterPro; IPR006264; AroC Ctransf.  
 DR InterPro; IPR001986; EPSP\_synth.  
 DR Pfam; PF00275; EPSP\_synthase; 1.  
 DR ProDom; PD001867; EPSP\_synth; 1.  
 DR TIGRFAMs; TIGR01356; aroA; 1.  
 DR PROSITE; PS00104; EPSP SYNTHASE 1; 1.  
 DR PROSITE; PS00885; EPSP SYNTHASE 2; 1.  
 KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;  
 KW Complete proteome; Transferase.  
 SQ SEQUENCE 445 AA; 46372 MW; C64A2896297F4B77 CRC64;

Query Match 54.7%; Score 1252.5; DB 2; Length 445;  
 Best Local Similarity 59.5%; Pred. No. 6.1e-67;  
 Matches 263; Conservative 52; Mismatches 116; Indels 11; Gaps 5;  
 QY 9 PATARKSSGLSGTVAIPGDKSISHRSFMFGLASGETRTITGLLEGEDVINTGKAMQAMGA 68  
 DB 9 PLQARKSGALHHTAVPDKSISHRALIIGALAVGSTRISGLLEGEDVINTKAMALGA 68  
 QY 69 RIRKESGD-TWIIDGVNGGLAPAPLDFGNATGCLTMGLGVVYDPDSTPIGDASLTR 127  
 DB 69 KYERTGDCEMRVHGVAVGAFATPEAPLDFGNAGTGCRLMAGVAGSPIVATFDGDASLSR 128  
 QY 128 RRMGRVLANPLREMGVQ-VKSEEDGRLPYTLRGPKTPTITRVPMASQAVKSAVLLAGLN 186  
 DB 129 RRMGRVLANPLREMGVQ-VKSEEDGRLPYTLRGPKTPTITRVPMASQAVKSAVLLAGLN 188  
 QY 187 TGTITVIEPIMTDRHTEKMLQGFANLTVETDADGV--RTIRLEGKSLTGVVIDVPGDP 244  
 DB 189 AGCITTVIAEASRDHTEMLQHFGA--TIVIEABAHARKISLTQPELRKAPVVPVD 246  
 QY 245 PSTAPFLVAALLVPGSDVTILNVLNMPRTGILITLQEMGADIEVINPRLAGGEDVADL 304  
 DB 247 PSTAPFLVAALLVPGSDITELTDMNPLRTGILITLRFMGASIEDSDVGDAGEPMARF 306  
 QY 305 RVRSSTLKGVTVPEDRAPSIMIDEYPILAVAAPFAEGATVWNGJLEELRVESRSLVANG 364  
 DB 307 RVRSSTLKGVEVPEDRAPSIMIDEYPILAVAAPFAEGATVWNGJLEELRVESRSLVANG 366  
 QY 365 LKLVGVDCEGETSLVVRGRPDGKLGASGAAVATHLDRILMSFLVWGLVSENPVTVD 424  
 DB 367 LRVNGVAVEIADDDLVBEKGHPG-----GGVAVTHMDHRIAMSLANGLASDKVTVTD 421  
 QY 425 DATMTATSPFEMDLNAGLAK 446

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DB      422 DTAFATSPDPEVPMQRIGAE 443

RESULT 12
AC      AROA BRAJA      STANDARD;      PRT;      469 AA.
ID      089WF2;
DT      10-OCT-2003 (Rel. 42, Created)
DT      10-OCT-2003 (Rel. 42, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
DE      enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPs).
GN      Name=aroA; OrderedLocustNames=blr0738;
OS      Bradyrhizobium japonicum.
OC      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC      Bradyrhizobiaceae; Bradyrhizobium.
OX      NCBI_TaxID=375;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=USDA 110;
RX      MEDLINE=22484998; PubMed=12597275;
RA      Kaneo T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,
RA      Sasamoto S., Watanabe A., Idegawa K., Iritani M., Kawashima K.,
RA      Kohara M., Matsunoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA      Tabata S.;
RT      "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT      Bradyrhizobium japonicum USDA110."
RL      DNA Res. 9:189-197(2002).
CC      -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC      phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC      -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC      sixth step.
CC      -1- SUBUNIT: Monomer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC      -1- SIMILARITY: Belongs to the EPSP synthase family.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; AP005937; BAC4603.1; -.
CC      DR      HAMAP; MF_00210; -.
CC      DR      InterPro; IPR006264; AroA.
CC      DR      InterPro; IPR001986; EPSP synth.
CC      DR      Pfam; PF00275; EPSP synthase; 1.
CC      DR      ProDom; PD001867; EPSP synth; 1.
CC      DR      PROSITE; PS00104; EPSP SYNTHASE_1; 1.
CC      DR      PROSITE; PS00885; EPSP SYNTHASE_2; 1.
CC      KW      Aromatic amino acid biosynthesis; Complete proteome; Transferase.
CC      SEQUENCE 469 AA; 48980 MW; DA55AA4F23BB85D5 CR64;

Query Match      53.7%; Score 1228.5; DB 1; Length 469;
Best Local Similarity 56.7%; Pred. No. 1.8e-65;
Matches 254; Conservative 60; Mismatches 127; Indels 7; Gaps 3;

QY      1 MHGASRPATARKSGSLGTRIGDCKSIHRSFMFGSLAGERRITGLGGEVINTG 60
DB      25 LHSQOPRLQSRANGPLTGKVRPEDKSISRALLGLAAGEYRISGLLEGEDVLTNA 84
QY      61 KAMQAMGARIRKEGD-TWIIIDGVNGGGLAPAPAPLDFFGNATGCRITWMLGVYDFDSTF 119
DB      85 KSMQGLGASVERTGPFAMKVGQVAVGAFQPKALDFGSGGCRILVMQAVAGCPSIAVF 144
QY      120 IGDASLTRPKGRVLANPLREMGVQYS-EDGRLPYTLRGKPTPIPTTYRVMAQAQYS 178
DB      145 DGDASIRSPKMRRIIDPLEKMGARVVSQGEGRLLPLTLGGADPLPITTYKTVAQAQYS 204
QY      179 AVLAGLMTPGITTYTIEPIMTEDHTEKMLQGFGANLTVETDADGVRTITLBERGLTQGV 238

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DB      205 AVLAGLAPGTTTYIESEASRDHTEMLKHPGADITSTKSGQRRTLVQGPRLHGAN 264
QY      239 IDVPDPSSTAFPLVALLVPGSDVTILNVLNMPRTGLITLQEMGADIEVINRLAG 298
DB      265 VVVPADPSAAPPVVAALIAEGSDVLSVMTNPFRTGLFTTLRMGASIESEVRGADG 324
QY      299 EDVADLRSSSTLKQVTPEDRAPSMIDEPYILANVAAPFAGATYMNGLERVYESRRL 358
DB      325 EPMQGLRVASRLKRVVEVPEPRAPSMIDEPYILAVVAAPFAGATTMRGLQELRVKESDRL 384
QY      359 SAVNGLKLVGDCBEGSTSLVVRGRPDGKIGNAGAAVATLDDHRITAMSFVLVGLVSE 418
DB      365 EATAMLVNKGKRVESGDDLVVQGRGVPG-----GGTVATHMHRITAMSLVWVGCSAD 439
QY      419 NEVTVDATMTATSPPEFMDIMAGIGAK 446
DB      440 QGVTVDDTAFATSPDPEFIPMWRISIGAE 467

RESULT 13
AC      AROA CAUCR      STANDARD;      PRT;      443 AA.
ID      09A2H2;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
DE      enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPs).
GN      Name=aroA; OrderedLocustNames=CC3589;
OS      Caulobacter crescentus.
OC      Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC      Caulobacteraceae; Caulobacter.
OX      NCBI_TaxID=155892;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 19089 / CB15;
RX      MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA      Nieren W.C., Feldberg T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA      Eilen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA      Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA      DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA      Kolonay J.F., Smit J., Craven M.B., Khouiri H.M., Sherry J.,
RA      Berry K.J., Uetzerback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA      Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA      Fraser C.M.;
RT      "Complete genome sequence of Caulobacter crescentus."
RL      Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC      -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC      phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC      -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC      sixth step.
CC      -1- SUBUNIT: Monomer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC      -1- SIMILARITY: Belongs to the EPSP synthase family.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; AB006017; AAK25551.1; -.
CC      DR      PIR; C87694; C87694.
CC      DR      TIGR; CC3589; -.
CC      DR      HAMAP; MF_00210; -.
CC      DR      InterPro; IPR006264; AroA.
CC      DR      InterPro; IPR001986; EPSP synth.
CC      DR      Pfam; PF00275; EPSP synthase; 1.
CC      DR      ProDom; PD001867; EPSP synth; 1.
CC      DR      TIGRfam; TIGR01356; aroA; 1.
CC      DR      PROSITE; PS00104; EPSP SYNTHASE_1; 1.

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DR PROSITE; PS00865; EPSP\_SYNTHASE\_2; FALSE\_NEG.  
 KM Aromatic amino acid biosynthesis; Complete proteome; Transferase.  
 SQ SEQUENCE 443 AA; 46075 MW; 458BA1463E10B6EC CRC64;

Query Match 49.6%; Score 1135; DB 1; Length 443;

Best Local Similarity 55.8%; Pred. No. 6,4e-60;  
 Matches 251; Conservative 45; Mismatches 138; Indels 16; Gaps 6;

QY 2 LKASSRPTARKSSGLSGTVRIIPGDKSISHRSFMFGASGETRTTGLLEGDDVINTK 61  
 DB 3 LKGLKAPAGCA-----LRGIVRAPGDKSISHRSMTIGALLTGTVEGLLEGDDVINTK 57  
 QY 62 AMQAMGARIRKESG-DTWIIDGVNGGLLPEAFLDFGNATGCRITMGLVGVYDPSTPI 120  
 DB 58 AMQAFARIREREGVGRIRIE--GKGFEPPVVDIDCGMGTGRILMGAAGRAMCATFT 115  
 QY 121 GDASTLRPMGRVLPDLREMGVQVKSSEDGRLPVTLRGPKPTPTITRYVPMASQVKSAY 180  
 DB 116 GQOSTLRGEMGRVLDPLARMGATWLGDRDKGRPLTLTKGNL--RGLNYTLPMASQVKSAY 174  
 QY 181 LLAGNTPGITTYIEPIMTDRHEKMLQGFANLTYETDADGVRT--IRLGRGLTQ 237  
 DB 175 LLAGLHAEAGVEVTEBEATRDHTRMLRAFGAEVIVEDRKAGDKTRHVRRLPEGQKLTGT 234  
 QY 238 VIDVPGDPSTAPFLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAG 297  
 DB 235 HVAVPEDPSSAFPLVAALIVPSESVTVSGVMNEIRLTGFTTLQEMGADIVISNVRVAS 294  
 QY 298 GEDVADLRVRSSTLKGVTVPEDRAPSMIDEPYLAVALAFAEGATVMNGLEELRYKESDR 357  
 DB 295 GSEVGDIRARYSQKGVVVPERAPSMIDEPYLAVALAFASETVMRGVGEKRVKESDR 354  
 QY 358 LSAVANGKLNVDCDEGETSLVVRGRPRGKLGNAAGAAVATHDRIAMSLVMGLVYS 417  
 DB 355 ISLTANGLACGVQVVEEPEGFIV---TGTGQPPKGAATVYVGHRIAMSLVIGMAA 410  
 QY 418 ENPVTVDDATMTATSPPEFMDLMAIGLAKI 447  
 DB 411 QAEVAVDEPGMTATSPFGADLMRGLGATL 440

## RESULT 14

QY 09H269 PRELIMINARY; PRT; 746 AA.  
 AC 09H269;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Still frameshift 3-PHOSPHOSHIMIMATE 1-CARBOXYVINYLTRANSFERASE  
 DE prephenate dehydrogenase.  
 GN OrderedLocuNames=PA3164;  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxId=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/5023079;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kae A., Larbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.,  
 RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen.";  
 RT Nature 406:959-964(2000).  
 CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =  
 CC phosphinate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.  
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;  
 CC sixth step.  
 CC -1- SIMILARITY: Belongs to the EPSP synthase family.

DR EMBL; AE004740; AAG06552.1; -.  
 DR PIR; B83250; B83250.  
 DR HSSP; Q9S400; 1RP4.  
 DR GO; GO:0003866; P:3-phosphoshikimate-1-carboxyvinyltransferase; .; IEA.  
 DR GO; GO:0004665; P:prephenate dehydrogenase (NADP+) activity; IEA.  
 DR GO; GO:0016740; P:transferrase activity; IEA.  
 DR GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh.; IEA.  
 DR GO; GO:0006571; P:tyrosine biosynthesis; IEA.  
 DR InterPro; IPR006264; AroC\_Ctransf.  
 DR InterPro; IPR001986; EPSP synth.  
 DR InterPro; IPR002025; NAD\_B5.  
 DR InterPro; IPR003099; Prephen\_déhydrog.  
 DR Pfam; PF00275; EPSP synthase; 1.  
 DR Pfam; PF02153; PDH; 1.  
 DR ProDom; PD001667; EPSP synth; 1.  
 DR TIGRfam; TIGR01356; atoa; 1.  
 DR PROSITE; PS00104; EPSP\_SYNTHASE\_1; 1.  
 DR PROSITE; PS00865; EPSP\_SYNTHASE\_2; 1.  
 KM Amino-acid biosynthesis; Aromatic amino acid biosynthesis;  
 KW Complete proteome; Transferase.  
 SQ SEQUENCE 746 AA; 79320 MW; C297484BF539E3A CRC64;

Query Match 43.2%; Score 989.5; DB 2; Length 746;  
 Best Local Similarity 48.5%; Pred. No. 5.9e-51;  
 Matches 214; Conservative 62; Mismatches 152; Indels 13; Gaps 3;

QY 12 ARKSSGLSGTVRIIPGDKSISHRSFMFGASGETRTTGLLEGDDVINTKAMQAMGARIR 71  
 DB 317 AOPGSLSGTIVIPGDKSISHRSIMGLSABGTTEVEGLLEGDDALATTQAFNDGVVIE 376  
 QY 72 -KEGDTWIIDGVNGGLLPEAFLDFGNATGCRITMGLVGVYDPSTPIGASLTGRPM 130  
 DB 377 GQNGKRVTVHGVGLKAPPGPIYVNGSTGMRLLSGLLAQPPSTLTGDAISLKRPM 436  
 QY 131 GVALNPLREMGVQVKSSEDGRLPVTLRGPKPTPTITRYVPMASQVKSAYVLLAGLTPGI 190  
 DB 437 NRVAPLRERMGAVIEGPEGRPPMTIRGGQRLTGKMHYDPMASQVKSAYVLLAGLTAAB 496  
 QY 191 TVIPIPIMTDRHEKMLQGFANLTYETDADGVRTIRLGRGLTQGVIVDPDPSTAP 250  
 DB 497 TSVTEPAPTRDHTERMLRGFGYVNVESG---TAKVSGHLSYTHLEVPADISSAF 551  
 QY 251 PLVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGSDVADLRVRSST 310  
 DB 552 FLVAASIAEGSELVIVOHGAINPTRVGVIETILMGDDLSLEQREVGEPVADIRRSAR 611  
 QY 311 LKGVTVPEDRAPSMIDEPYLAVALAFAEGATVMNGLEELRYKESDRLSAVANGKLNGV 370  
 DB 612 LKSIDIPEDLVPLAIDEPFVLFAVAAACABGRVTLRGAELRYKESDRIOVMADGLKALGV 671  
 QY 371 DCDDEGETSLVVRGRPRGKLGNAAGAAVATHDRIAMSLVMGLVSENPVYDDATMTA 430  
 DB 672 KAEPTPDGIVIG-----GAFGGGEVWAHGDHRIAMSLVSAASPIRIRHDCANVA 724  
 QY 431 TSFPEFMDLMAIGAKIELSD 451  
 DB 725 TSFPEFMDLCAQTGRVAVEN 745

## RESULT 15

QY 088M05 PRELIMINARY; PRT; 746 AA.  
 AC 088M05;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Prephenate dehydrogenase, putative/3-phosphoshikimate 1-  
 DE carboxyvinyltransferase.  
 GN OrderedLocuNames=ppi1770;  
 OS Pseudomonas putida (strain KT2440).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxId=160488;

RP [1]  
SEQUENCE FROM N.A.  
RX MEDLINE=22423060; PubMed=12534463;  
RA Nelson K.E., Weiner C., Paulsen I.T., Dodson R.J., Hilbert H.,  
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,  
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,  
RA Madupu R., Nelson W.C., White O., Peterson J.D., Kouri H.M.,  
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,  
RA Moazzez A., Uterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,  
RA Medler H., Lauber J., Stjepandic D., Hohsels J., Straetz M., Heim S.,  
RA Kiewitz C., Eissen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,  
RA Fraser C.M.;  
RT "Complete genome sequence and comparative analysis of the  
RT metabolically versatile Pseudomonas putida KT2440.";  
RL Environ. Microbiol. 4:799-808 (2002).  
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =  
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.  
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;  
CC sixth step.  
CC -1- SIMILARITY: Belongs to the EPSP synthase family.  
CC  
DR HMBL; AB016780; AAN67390.1; -.  
DR HSSP; Q9S400; 1RF4.  
DR TIGR; P1770; -.  
DR GO; GO:0003866; F:3-phosphoshikimate 1-carboxyvinyltransferase. . .; IEA.  
DR GO; GO:0004665; F:isoprenate dehydrogenase (NADP+) activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0016089; P:aromatic amino acid family biosynthesis. sh. . .; IEA.  
DR GO; GO:0006571; P:tyrosine biosynthesis; IEA.  
DR InterPro; IPR006264; AroA Ctransf.  
DR InterPro; IPR001986; EPSP synth.  
DR InterPro; IPR000205; NAD\_B.  
DR InterPro; IPR003099; Prephen dehydrog.  
DR Pfam; PF00275; EPSP\_synthase; 1.  
DR Pfam; PF02153; PDH; 1.  
DR ProDom; PD001867; EPSP synth; 1.  
DR TIGRFAMs; TIGR01356; aroA; 1.  
DR PROSITE; PS00104; EPSP\_SYNTHASE\_1; 1.  
DR PROSITE; PS00885; EPSP\_SYNTHASE\_2; 1.  
DR Amino-acid biosynthesis; Aromatic amino acid biosynthesis;  
DR Complete proteome; Transferase.  
DR KW  
SQ SEQUENCE 746 AA; 79133 MW; 7148AA1B4DDC1AB2 CRC64;

Query Match 42.4%; Score 970.5; DB 2; Length 746;  
Best Local Similarity 49.2%; Pred. No. 8e-50;  
Matches 216; Conservative 57; Mismatches 149; Indels 17; Gaps 5;

QY 12 ARKSSGLSGTVRIIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTGKAMQAMGARIR 71  
DB 316 AQPGRGLNRIRIVPDGKSIHSIMGLSABEGTTEVEGFLGEDALATTQAFRDMGVLI- 374  
QY 72 KEGDTW--IIDGVNGGLLAEAPLDFGNAAATGCRLTGMLGVGVYDFDSTFTIGDASLTKR 128  
DB 375 -EGPNHGRVTLHGVLGHGLKPPGPGPLVNGSGTSMRLLSGLLAGCPFDVTMTGDASLSKR 433  
QY 129 PMGRVLNPLREMGVOYKSDGRLPVTLAGPKTPPTITRVPMASQOVSAVLGALNTP 188  
DB 434 PMNRVANPLREMGAAVETGDPDRPPLTIRGHLKGLTYTLTPWASAQVRSCLLAGLYAE 493  
QY 189 GITTVEPIMTDHEKMLQGFANLTVETDADGVRTIRLEGRGKLTGQVIDVPDPSST 248  
DB 494 GKITVTERPAPTDHTRMLRGFGYSV---DSHG-PVASLQSGKLTATRIEVPADISSA 548  
QY 249 APFLVAALLVPGSDVTILNVLNMPRTGLITLQEMGADIEVINPRLAGEEDVADLRVS 308  
DB 549 APFLVAASIAEGSELVLEHVGINPRTGVIDILRLMGDITLENQREVGEPVADLRVG 608  
QY 309 STLKGVTVPEDEAPSMIDEXPLIAVAAAFAGATVNGLELRVKSDDLAVANGKLIN 368  
DB 609 ALKKGIDIPLEALVPLAIDEPVLFVAACAEGRTVLRGAEELRVKSDDRIQWADGLTTL 668  
QY 369 GVDCEGETSLVVRGPRDGKLGNSGAVAATHLDRIMSFVWGLVSENPTVDDATM 428  
DB 669 GIKCEPTPDGIIIDG-----QMGGGEVHGHRIMAFSVASLRASAPRIHDCAN 721

QY 429 IATSFPEPMIDMAGIGAKI 447  
DB 722 VATSPFNPLALCAEVGIRV 740  
Search completed: April 20, 2005, 15:25:50  
Job time : 75 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 20, 2005, 15:23:22 ; Search time 139 Seconds  
(without alignments)  
1087.976 Million cell updates/sec

Title: US-10-622-201-70

Perfect score: 2288  
Sequence: 1.MHGA5RPARFARKSSGLSG.....FMDLMAGLGAETLSDTYAA 455

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2288	100.0	455	9	US-09-861-696-70
2	2288	100.0	455	9	US-09-464-099A-70
3	2282	99.7	455	9	US-09-861-696-3
4	2282	99.7	455	9	US-09-464-099A-3
5	2271	99.3	524	15	US-10-424-599-169346
6	1900.5	83.1	449	9	US-09-861-696-5
7	1900.5	83.1	449	9	US-09-861-696-7
8	1900.5	83.1	449	9	US-09-464-099A-5
9	1900.5	83.1	449	9	US-09-464-099A-7
10	1855.5	81.1	480	14	US-10-214-766-30
11	1783	77.9	452	15	US-10-369-493-12116
12	1233.5	53.9	430	15	US-10-369-493-20766
13	1213.5	53.0	432	15	US-10-369-493-10476

14	1188.5	51.9	418	15	US-10-369-493-7814	Sequence 7814, Ap
15	1149.5	50.2	420	15	US-10-369-493-18039	Sequence 18039, A
16	1135	49.6	443	15	US-10-369-493-17074	Sequence 17074, A
17	983	43.0	411	15	US-10-369-493-9974	Sequence 9974, Ap
18	927.5	40.5	442	15	US-10-369-493-15383	Sequence 15383, A
19	912.5	39.9	454	15	US-10-369-493-17730	Sequence 17730, A
20	908.5	39.7	408	15	US-10-369-493-9302	Sequence 9302, Ap
21	908.5	39.7	412	15	US-10-369-493-9499	Sequence 9499, Ap
22	906.5	39.6	408	15	US-10-369-493-15751	Sequence 15751, A
23	906.5	39.6	408	15	US-10-369-493-16135	Sequence 16135, A
24	864	38.6	431	15	US-10-369-493-17242	Sequence 17242, A
25	878	38.4	675	15	US-10-369-493-13934	Sequence 13934, A
26	867.5	37.9	447	9	US-09-861-696-67	Sequence 67, Appl
27	867.5	37.9	447	9	US-09-464-099A-67	Sequence 67, Appl
28	867.5	37.9	447	15	US-10-369-493-2764	Sequence 2764, Ap
29	835.5	36.5	424	15	US-10-369-493-20917	Sequence 20917, A
30	834.5	36.5	417	15	US-10-369-493-9745	Sequence 9745, Ap
31	806.5	35.2	430	15	US-10-369-493-18482	Sequence 18482, A
32	806	35.2	443	9	US-09-861-696-69	Sequence 69, Appl
33	806	35.2	443	9	US-09-464-099A-69	Sequence 69, Appl
34	806	35.2	443	14	US-10-214-766-31	Sequence 31, Appl
35	803.5	35.1	417	15	US-10-369-493-16494	Sequence 16494, A
36	803.5	35.1	427	17	US-10-472-928-2780	Sequence 2780, Ap
37	787	34.4	424	15	US-10-369-493-8970	Sequence 8970, Ap
38	785	34.3	428	9	US-09-861-696-42	Sequence 42, Appl
39	785	34.3	428	9	US-09-464-099A-42	Sequence 42, Appl
40	785	34.3	428	15	US-10-369-493-23174	Sequence 23174, A
41	766.5	33.5	431	15	US-10-369-493-113	Sequence 113, App
42	695	30.4	410	15	US-10-369-493-2931	Sequence 2931, Ap
43	577	25.2	430	9	US-09-861-696-44	Sequence 44, Appl
44	577	25.2	430	9	US-09-464-099A-44	Sequence 44, Appl
45	521.5	22.8	429	15	US-10-335-977-6495	Sequence 6495, Ap

## ALIGNMENTS

RESULT 1  
US-09-861-696-70  
Sequence 70, Application US/09861696  
Patent No. US20020007053A1  
GENERAL INFORMATION:  
APPLICANT: Barry, Gerard F.  
APPLICANT: Padgett, Stephen R.  
APPLICANT: Stallings, William C.  
TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES  
FILE REFERENCE: 11899.0175.CNUS04 MOBT:175-4  
CURRENT APPLICATION NUMBER: US/09/861,696  
CURRENT FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: US 09/137,440  
PRIOR FILING DATE: 1998-08-20  
PRIOR APPLICATION NUMBER: US 08/833,485  
PRIOR FILING DATE: 1997-04-07  
PRIOR APPLICATION NUMBER: US 08/306,063  
PRIOR FILING DATE: 1994-09-13  
PRIOR APPLICATION NUMBER: US 07/749,611  
PRIOR FILING DATE: 1991-08-28  
PRIOR APPLICATION NUMBER: US 07/576,537  
PRIOR FILING DATE: 1990-08-31  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 70  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-861-696-70  
Query Match 100.0%; Score 2288; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 7.4e-182;  
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHGASSRPATARKSSGSLGTVRIPGDKSISHRSFMEFGGLASGETRITGLLEGEDVINTG 60  
DB 1 MHGASSRPATARKSSGSLGTVRIPGDKSISHRSFMEFGGLASGETRITGLLEGEDVINTG 60  
QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLDFGNAAATGCRITMGLVGYDDPSTFI 120  
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QY 121 GDSALTKRPMGRVLPNLEMEGVQVKSSEDGRLPVTLRGPKPTPTITTYRVPMAAQVKSAY 180  
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QY 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFANLIVETDAGVRIIRLEGKLTGOVID 240  
DB 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFANLIVETDAGVRIIRLEGKLTGOVID 240  
QY 241 VPGDSSSTAFPLVALLVPGSDVTILNVLNMPTRGLITLQEMGADIEVINPRLAGGED 300  
DB 241 VPGDSSSTAFPLVALLVPGSDVTILNVLNMPTRGLITLQEMGADIEVINPRLAGGED 300  
QY 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYILAFAAFAEGATVMNGLEELRYKESDRLSA 360  
DB 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYILAFAAFAEGATVMNGLEELRYKESDRLSA 360  
QY 361 VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAATAVTHLDRIRIAMSFLVMGLVSENP 420  
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QY 421 VTVDATMIATSFPEFMDLMAGLAKIELSDTKAA 455  
DB 421 VTVDATMIATSFPEFMDLMAGLAKIELSDTKAA 455

RESULT 2  
US-09-464-099A-70  
; Sequence 70, Application US/09464099A  
; Patent No. US20020168680A1  
; GENERAL INFORMATION:  
; APPLICANT: Barry, Gerard F.  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Padgett, Stephen R.  
; APPLICANT: Stallings, William C.  
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOCLPYUVULSHIKIMATE-3-PHOSPHATE SYNTHASES  
; FILE REFERENCE: 11899.0175.CNUS01 MOBT:175-2  
; CURRENT APPLICATION NUMBER: US/09/464,099A  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: US 09/137,440  
; PRIOR FILING DATE: 1998-08-20  
; PRIOR APPLICATION NUMBER: US 08/833,485  
; PRIOR FILING DATE: 1997-04-07  
; PRIOR APPLICATION NUMBER: US 08/306,063  
; PRIOR FILING DATE: 1994-09-13  
; PRIOR APPLICATION NUMBER: US 07/749,611  
; PRIOR FILING DATE: 1991-08-28  
; PRIOR APPLICATION NUMBER: US 07/576,537  
; PRIOR FILING DATE: 1990-08-31  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 70  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-464-099A-70

Query Match 100.0%; Score 2288; DB 9; Length 455;  
Best Local Similarity 100.0%; Pred. No. 7.4e-182;  
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MHGASSRPATARKSSGSLGTVRIPGDKSISHRSFMEFGGLASGETRITGLLEGEDVINTG 60

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QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLDFGNAAATGCRITMGLVGYDDPSTFI 120  
DB 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLDFGNAAATGCRITMGLVGYDDPSTFI 120  
QY 121 GDSALTKRPMGRVLPNLEMEGVQVKSSEDGRLPVTLRGPKPTPTITTYRVPMAAQVKSAY 180  
DB 121 GDSALTKRPMGRVLPNLEMEGVQVKSSEDGRLPVTLRGPKPTPTITTYRVPMAAQVKSAY 180  
QY 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFANLIVETDAGVRIIRLEGKLTGOVID 240  
DB 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFANLIVETDAGVRIIRLEGKLTGOVID 240  
QY 241 VPGDSSSTAFPLVALLVPGSDVTILNVLNMPTRGLITLQEMGADIEVINPRLAGGED 300  
DB 241 VPGDSSSTAFPLVALLVPGSDVTILNVLNMPTRGLITLQEMGADIEVINPRLAGGED 300  
QY 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYILAFAAFAEGATVMNGLEELRYKESDRLSA 360  
DB 301 VADLRVRSSTLKGVTVPEDRAPSMIDEPYILAFAAFAEGATVMNGLEELRYKESDRLSA 360  
QY 361 VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAATAVTHLDRIRIAMSFLVMGLVSENP 420  
DB 361 VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAATAVTHLDRIRIAMSFLVMGLVSENP 420  
QY 421 VTVDATMIATSFPEFMDLMAGLAKIELSDTKAA 455  
DB 421 VTVDATMIATSFPEFMDLMAGLAKIELSDTKAA 455

RESULT 3  
US-09-861-696-3  
; Sequence 3, Application US/09861696  
; Patent No. US20020007053A1  
; GENERAL INFORMATION:  
; APPLICANT: Barry, Gerard F.  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Padgett, Stephen R.  
; APPLICANT: Stallings, William C.  
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOCLPYUVULSHIKIMATE-3-PHOSPHATE SYNTHASES  
; FILE REFERENCE: 11899.0175.CNUS04 MOBT:175-4  
; CURRENT APPLICATION NUMBER: US/09/861,696  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: US 09/137,440  
; PRIOR FILING DATE: 1998-08-20  
; PRIOR APPLICATION NUMBER: US 08/833,485  
; PRIOR FILING DATE: 1997-04-07  
; PRIOR APPLICATION NUMBER: US 08/306,063  
; PRIOR FILING DATE: 1994-09-13  
; PRIOR APPLICATION NUMBER: US 07/749,611  
; PRIOR FILING DATE: 1991-08-28  
; PRIOR APPLICATION NUMBER: US 07/576,537  
; PRIOR FILING DATE: 1990-08-31  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Agrobacterium sp.  
US-09-861-696-3

Query Match 99.7%; Score 2282; DB 9; Length 455;  
Best Local Similarity 99.8%; Pred. No. 2.3e-181;  
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MHGASSRPATARKSSGSLGTVRIPGDKSISHRSFMEFGGLASGETRITGLLEGEDVINTG 60  
DB 1 MHGASSRPATARKSSGSLGTVRIPGDKSISHRSFMEFGGLASGETRITGLLEGEDVINTG 60  
QY 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLDFGNAAATGCRITMGLVGYDDPSTFI 120  
DB 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLDFGNAAATGCRITMGLVGYDDPSTFI 120



QY 121 GDASLTKEPMGKVLNPLREMGVQVKSSEDGRLPVTLRGKPTPTPIYRVPMASAOVKSAY 180  
DB 121 GDASLTKEPMGKVLNPLREMGVQVKSSEDGRLPVTLRGKPTPTPIYRVPMASAOVKSAY 180  
QY 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGKGLTGQVID 240  
DB 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGKGLTGQVID 240  
QY 241 VGDSSSTAFPLVAALLVPGSDVTILNVLNMPTRGILLTLOEMGADIEVINPRLAGSD 300  
DB 241 VGDSSSTAFPLVAALLVPGSDVTILNVLNMPTRGILLTLOEMGADIEVINPRLAGSD 300  
QY 301 VADLRVRSSTLKGVTVPEEDRAPSMIDEYPIILVAAAFAGATVMNGLEELRYKESDRLSA 360  
DB 301 VADLRVRSSTLKGVTVPEEDRAPSMIDEYPIILVAAAFAGATVMNGLEELRYKESDRLSA 360  
QY 361 VANGKLKLVGDCDEGETSLVVRGPRDGKGLGNASGAANAVALTHDRIAMSLVMGLVSENP 420  
DB 361 VANGKLKLVGDCDEGETSLVVRGPRDGKGLGNASGAANAVALTHDRIAMSLVMGLVSENP 420  
QY 421 VTVDATMTATSPPEFMDLMAGLGAKIELSDTKAA 455  
DB 421 VTVDATMTATSPPEFMDLMAGLGAKIELSDTKAA 455

## RESULT 4

US-09-464-099A-3  
; Sequence 3, Application US/09464099A  
; Patent No. US20020168680A1  
; GENERAL INFORMATION:  
; APPLICANT: Barry, Gerard F.  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Padgett, Stephen R.  
; APPLICANT: Stallings, William C.  
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOPIRYVUVYSHIKIMATE-3-PHOSPHATE SYNTHASES  
; FILE REFERENCE: 11899.0175.CNISO1 MOST:175-2  
; CURRENT APPLICATION NUMBER: US/09/464,099A  
; CURRENT FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: US 09/137,440  
; PRIOR FILING DATE: 1998-08-20  
; PRIOR APPLICATION NUMBER: US 08/833,485  
; PRIOR FILING DATE: 1997-04-07  
; PRIOR APPLICATION NUMBER: US 08/306,063  
; PRIOR FILING DATE: 1994-09-13  
; PRIOR APPLICATION NUMBER: US 07/749,611  
; PRIOR FILING DATE: 1991-08-28  
; PRIOR APPLICATION NUMBER: US 07/576,537  
; PRIOR FILING DATE: 1990-08-31  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 3  
; LENGTH: 455  
; TYPE: PRF  
; ORGANISM: Agrobacterium sp.  
US-09-464-099A-3

Query Match 99.7%; Score 2282; DB 9; Length 455;  
Best Local Similarity 99.8%; Pred. No. 2,3e-181;  
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHGASSRPATARKSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
DB 1 MHGASSRPATARKSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
QY 61 KAMQAMGARIRKEDGTWIIDGVNGGLAPEAPLDFGNATGCRITMGLVGVPDSTFI 120  
DB 61 KAMQAMGARIRKEDGTWIIDGVNGGLAPEAPLDFGNATGCRITMGLVGVPDSTFI 120  
QY 121 GDASLTKEPMGKVLNPLREMGVQVKSSEDGRLPVTLRGKPTPTPIYRVPMASAOVKSAY 180  
DB 121 GDASLTKEPMGKVLNPLREMGVQVKSSEDGRLPVTLRGKPTPTPIYRVPMASAOVKSAY 180

QY 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGKGLTGQVID 240  
DB 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGKGLTGQVID 240  
QY 241 VGDSSSTAFPLVAALLVPGSDVTILNVLNMPTRGILLTLOEMGADIEVINPRLAGSD 300  
DB 241 VGDSSSTAFPLVAALLVPGSDVTILNVLNMPTRGILLTLOEMGADIEVINPRLAGSD 300  
QY 301 VADLRVRSSTLKGVTVPEEDRAPSMIDEYPIILVAAAFAGATVMNGLEELRYKESDRLSA 360  
DB 301 VADLRVRSSTLKGVTVPEEDRAPSMIDEYPIILVAAAFAGATVMNGLEELRYKESDRLSA 360  
QY 361 VANGKLKLVGDCDEGETSLVVRGPRDGKGLGNASGAANAVALTHDRIAMSLVMGLVSENP 420  
DB 361 VANGKLKLVGDCDEGETSLVVRGPRDGKGLGNASGAANAVALTHDRIAMSLVMGLVSENP 420  
QY 421 VTVDATMTATSPPEFMDLMAGLGAKIELSDTKAA 455  
DB 421 VTVDATMTATSPPEFMDLMAGLGAKIELSDTKAA 455

## RESULT 5

US-10-424-599-169346  
; Sequence 169346, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J  
; APPLICANT: Kovalic, David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53223) B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 169346  
; LENGTH: 524  
; TYPE: PRF  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_123934C.1.dep  
US-10-424-599-169346

Query Match 99.3%; Score 2271; DB 15; Length 524;  
Best Local Similarity 99.8%; Pred. No. 2,4e-180;  
Matches 451; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHGASSRPATARKSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
DB 1 MHGASSRPATARKSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
QY 61 KAMQAMGARIRKEDGTWIIDGVNGGLAPEAPLDFGNATGCRITMGLVGVPDSTFI 120  
DB 61 KAMQAMGARIRKEDGTWIIDGVNGGLAPEAPLDFGNATGCRITMGLVGVPDSTFI 120  
QY 121 GDASLTKEPMGKVLNPLREMGVQVKSSEDGRLPVTLRGKPTPTPIYRVPMASAOVKSAY 180  
DB 121 GDASLTKEPMGKVLNPLREMGVQVKSSEDGRLPVTLRGKPTPTPIYRVPMASAOVKSAY 180  
QY 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGKGLTGQVID 240  
DB 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFANLTVETDADGVRTIRLEGKGLTGQVID 240  
QY 241 VGDSSSTAFPLVAALLVPGSDVTILNVLNMPTRGILLTLOEMGADIEVINPRLAGSD 300  
DB 241 VGDSSSTAFPLVAALLVPGSDVTILNVLNMPTRGILLTLOEMGADIEVINPRLAGSD 300  
QY 301 VADLRVRSSTLKGVTVPEEDRAPSMIDEYPIILVAAAFAGATVMNGLEELRYKESDRLSA 360  
DB 301 VADLRVRSSTLKGVTVPEEDRAPSMIDEYPIILVAAAFAGATVMNGLEELRYKESDRLSA 360  
QY 373 VADLRVRSSTLKGVTVPEEDRAPSMIDEYPIILVAAAFAGATVMNGLEELRYKESDRLSA 432  
DB 373 VADLRVRSSTLKGVTVPEEDRAPSMIDEYPIILVAAAFAGATVMNGLEELRYKESDRLSA 432  
QY 361 VANGKLKLVGDCDEGETSLVVRGPRDGKGLGNASGAANAVALTHDRIAMSLVMGLVSENP 420

Db 433 VANGKJNGVDCDEGETSLVVRGRPDGKGLGNASGAGVATHDRIAMSLVMGLVSENP 492  
Qy 421 VTVDATMIATSFPEFMDLMAIGAKIELSDT 452  
Db 493 VTVDATMIATSFPEFMDLMAIGAKIELSDT 524  
RESULT 6  
US-09-861-696-5  
; Sequence 5, Application US/09861696  
; Patent No. US20020007053A1  
; GENERAL INFORMATION:  
; APPLICANT: Barry, Gerard F.  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Padgett, Stephen R.  
; APPLICANT: Stallings, William C.  
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOPIRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES  
; FILE REFERENCE: 11899, 0175, CUS04 MOBT:175-4  
; CURRENT APPLICATION NUMBER: US/09/861,696  
; CURRENT FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: US 09/137,440  
; PRIOR FILING DATE: 1998-08-20  
; PRIOR APPLICATION NUMBER: US 08/833,485  
; PRIOR FILING DATE: 1997-04-07  
; PRIOR APPLICATION NUMBER: US 08/306,063  
; PRIOR FILING DATE: 1994-09-13  
; PRIOR APPLICATION NUMBER: US 07/749,611  
; PRIOR FILING DATE: 1991-08-28  
; PRIOR APPLICATION NUMBER: US 07/576,537  
; PRIOR FILING DATE: 1990-08-31  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Agrobacterium sp.  
US-09-861-696-5  
Query Match 83.1%; Score 1900.5; DB 9; Length 449;  
Best Local Similarity 82.9%; Pred. No. 1.4e-149;  
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;  
Qy 1 MHHGSSRPATARKSSGLSGTVIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
Db 1 MSHSASPPKATRRSEALTGIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
Qy 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPLPAFLDIFGNATGCRITMGLVGYDDPSFTI 120  
Db 61 RAMQAMGAKIRKEGDTWIIDGVNGGLAPLPAFLDIFGNATGCRITMGLVGYDDPSFTI 120  
Qy 121 GDASLTKRPMGRVNLPLREMGVQVXSEDDRLPVTLRGPKTPTPTTYRVPMASQVKSAY 180  
Db 121 GDASLTKRPMGRVNLPLREMGVQVXSEDDRLPVTLRGPKTPTPTTYRVPMASQVKSAY 180  
Qy 121 GPASLTKRPMGRVNLPLREMGVQVXSEDDRLPVTLRGPKTPTPTTYRVPMASQVKSAY 180  
Db 121 GPASLTKRPMGRVNLPLREMGVQVXSEDDRLPVTLRGPKTPTPTTYRVPMASQVKSAY 180  
Qy 181 LLAGINTPGITTVIPIRMDHTEKMLQGFANLTVETDAGVRTIRLEGKLTGVQYID 240  
Db 181 LLAGINTPGITTVIPIRMDHTEKMLQGFANLTVETDAGVRTIRLEGKLTGVQYID 240  
Qy 181 LLAGINTPGITTVIPIRMDHTEKMLQGFANLTVETDAGVRTIRLEGKLTGVQYID 240  
Db 181 LLAGINTPGITTVIPIRMDHTEKMLQGFANLTVETDAGVRTIRLEGKLTGVQYID 240  
Qy 241 VPGDSSSTAFPLVALLVPGSDVTILNVLMNPTRTGLITLQEMGADIEVINPRLAGGED 300  
Db 241 VPGDSSSTAFPLVALLVPGSDVTILNVLMNPTRTGLITLQEMGADIEVINPRLAGGED 300  
Qy 301 VADLVRASSTLKGTVVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLEELRYKESDRLSA 360  
Db 301 VADLVRASSTLKGTVVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLEELRYKESDRLSA 360  
Qy 301 VADLVRASSTLKGTVVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLEELRYKESDRLSA 360  
Db 301 VADLVRASSTLKGTVVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLEELRYKESDRLSA 360  
Qy 361 VANGKJNGVDCDEGETSLVVRGRPDGKGLGNASGAGVATHDRIAMSLVMGLVSENP 420  
Db 361 VANGKJNGVDCDEGETSLVVRGRPDGKGLGNASGAGVATHDRIAMSLVMGLVSENP 420  
Qy 361 VARGLEANGVDCDEGETSLVVRGRPDGKGLGNASGAGVATHDRIAMSLVMGLVSENP 420  
Db 361 VARGLEANGVDCDEGETSLVVRGRPDGKGLGNASGAGVATHDRIAMSLVMGLVSENP 420  
Qy 421 VTVDATMIATSFPEFMDLMAIGAKIELS 450  
Db 421 VTVDATMIATSFPEFMDLMAIGAKIELS 450

Db 418 VTVDSSNMIAATSFPEFMDMPLGAKIELS 447  
RESULT 7  
US-09-861-696-7  
; Sequence 7, Application US/09861696  
; Patent No. US20020007053A1  
; GENERAL INFORMATION:  
; APPLICANT: Barry, Gerard F.  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Padgett, Stephen R.  
; APPLICANT: Stallings, William C.  
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOPIRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES  
; FILE REFERENCE: 11899, 0175, CUS04 MOBT:175-4  
; CURRENT APPLICATION NUMBER: US/09/861,696  
; CURRENT FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: US 09/137,440  
; PRIOR FILING DATE: 1998-08-20  
; PRIOR APPLICATION NUMBER: US 08/833,485  
; PRIOR FILING DATE: 1997-04-07  
; PRIOR APPLICATION NUMBER: US 08/306,063  
; PRIOR FILING DATE: 1994-09-13  
; PRIOR APPLICATION NUMBER: US 07/749,611  
; PRIOR FILING DATE: 1991-08-28  
; PRIOR APPLICATION NUMBER: US 07/576,537  
; PRIOR FILING DATE: 1990-08-31  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Pseudomonas sp.  
US-09-861-696-7  
Query Match 83.1%; Score 1900.5; DB 9; Length 449;  
Best Local Similarity 82.9%; Pred. No. 1.4e-149;  
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;  
Qy 1 MHHGSSRPATARKSSGLSGTVIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
Db 1 MSHSASPPKATRRSEALTGIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
Qy 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPLPAFLDIFGNATGCRITMGLVGYDDPSFTI 120  
Db 61 RAMQAMGAKIRKEGDTWIIDGVNGGLAPLPAFLDIFGNATGCRITMGLVGYDDPSFTI 120  
Qy 121 GDASLTKRPMGRVNLPLREMGVQVXSEDDRLPVTLRGPKTPTPTTYRVPMASQVKSAY 180  
Db 121 GDASLTKRPMGRVNLPLREMGVQVXSEDDRLPVTLRGPKTPTPTTYRVPMASQVKSAY 180  
Qy 121 GPASLTKRPMGRVNLPLREMGVQVXSEDDRLPVTLRGPKTPTPTTYRVPMASQVKSAY 180  
Db 121 GPASLTKRPMGRVNLPLREMGVQVXSEDDRLPVTLRGPKTPTPTTYRVPMASQVKSAY 180  
Qy 181 LLAGINTPGITTVIPIRMDHTEKMLQGFANLTVETDAGVRTIRLEGKLTGVQYID 240  
Db 181 LLAGINTPGITTVIPIRMDHTEKMLQGFANLTVETDAGVRTIRLEGKLTGVQYID 240  
Qy 181 LLAGINTPGITTVIPIRMDHTEKMLQGFANLTVETDAGVRTIRLEGKLTGVQYID 240  
Db 181 LLAGINTPGITTVIPIRMDHTEKMLQGFANLTVETDAGVRTIRLEGKLTGVQYID 240  
Qy 241 VPGDSSSTAFPLVALLVPGSDVTILNVLMNPTRTGLITLQEMGADIEVINPRLAGGED 300  
Db 241 VPGDSSSTAFPLVALLVPGSDVTILNVLMNPTRTGLITLQEMGADIEVINPRLAGGED 300  
Qy 301 VADLVRASSTLKGTVVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLEELRYKESDRLSA 360  
Db 301 VADLVRASSTLKGTVVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLEELRYKESDRLSA 360  
Qy 301 VADLVRASSTLKGTVVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLEELRYKESDRLSA 360  
Db 301 VADLVRASSTLKGTVVPEDRAPSMIDEYPIILAVAAFAEGATVMNGLEELRYKESDRLSA 360  
Qy 361 VANGKJNGVDCDEGETSLVVRGRPDGKGLGNASGAGVATHDRIAMSLVMGLVSENP 420  
Db 361 VANGKJNGVDCDEGETSLVVRGRPDGKGLGNASGAGVATHDRIAMSLVMGLVSENP 420  
Qy 361 VARGLEANGVDCDEGETSLVVRGRPDGKGLGNASGAGVATHDRIAMSLVMGLVSENP 420  
Db 361 VARGLEANGVDCDEGETSLVVRGRPDGKGLGNASGAGVATHDRIAMSLVMGLVSENP 420  
Qy 421 VTVDATMIATSFPEFMDLMAIGAKIELS 450  
Db 421 VTVDATMIATSFPEFMDLMAIGAKIELS 450  
RESULT 8  
US-09-464-099A-5

Sequence 5, Application US/09464099A  
Patent No. US20020168680A1  
GENERAL INFORMATION:  
APPLICANT: Barry, Gerard F.  
APPLICANT: Kishore, Ganesh M.  
APPLICANT: Padgett, Stephen R.  
APPLICANT: Stallings, William C.  
TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES  
FILE REFERENCE: 11899.0175.CNISO1 MOBT:175-2  
CURRENT APPLICATION NUMBER: US/09/464,099A  
CURRENT FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: US 09/137,440  
PRIOR FILING DATE: 1998-08-20  
PRIOR APPLICATION NUMBER: US 08/833,485  
PRIOR FILING DATE: 1997-04-07  
PRIOR APPLICATION NUMBER: US 08/306,063  
PRIOR FILING DATE: 1994-09-13  
PRIOR APPLICATION NUMBER: US 07/749,611  
PRIOR FILING DATE: 1991-08-28  
PRIOR APPLICATION NUMBER: US 07/576,537  
PRIOR FILING DATE: 1990-08-31  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 5  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Agrobacterium sp.  
US-09-464-099A-5

Query Match 83.1%; Score 1900.5; DB 9; Length 449;  
Best Local Similarity 82.9%; Pred. No. 1.4e-149;  
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

QY 1 MHGASSRPATARKSSGLSGTVIRIPGDKSISHSRSMFGGLASGETRITGLBSEDVINTG 60  
DB 1 MSHSASPKPATARRSALTGEIRIPGDKSISHSRSMFGGLASGETRITGLBSEDVINTG 60  
QY 61 KMOAMGAKIRKRGDWTIIDVNGGGLAPAPLDPGNATGRLTMGLVGVYDFPSTFI 120  
DB 61 RAMQAMGAKIRKRGDWTIIDVNGGGLAPAPLDPGNATGRLTMGLVGVYDFPSTFI 120  
QY 121 GDSLTKRPMGRVNLPLREMGVQVKSDEGDRPLVTLRGKPTPTITRYVPMASQVKSAN 180  
DB 121 GDSLTKRPMGRVNLPLREMGVQVKSDEGDRPLVTLRGKPTPTITRYVPMASQVKSAN 180  
QY 121 GDSLTKRPMGRVNLPLREMGVQVKSDEGDRPLVTLRGKPTPTITRYVPMASQVKSAN 180  
DB 121 GDSLTKRPMGRVNLPLREMGVQVKSDEGDRPLVTLRGKPTPTITRYVPMASQVKSAN 180  
QY 181 LLAGLNTPGITTYIEBIMTRDHEKMLQGFGANLTYETDADGVRTIRLBGRKLTQVVD 240  
DB 181 LLAGLNTPGITTYIEBIMTRDHEKMLQGFGANLTYETDADGVRTIRLBGRKLTQVVD 240  
QY 241 VEGDPESTAFPLVAALLVGSQVTLINVLNMPRTGILLTLOEMGADIEVINRLAGGED 300  
DB 241 VEGDPESTAFPLVAALLVGSQVTLINVLNMPRTGILLTLOEMGADIEVINRLAGGED 300  
QY 301 VADLRVRSSTLKGVTPEDRAPSMIDEPYLAFAAFAEGATVMNGLEELRVKESDRLSA 360  
DB 301 VADLRVRSSTLKGVTPEDRAPSMIDEPYLAFAAFAEGATVMNGLEELRVKESDRLSA 360  
QY 361 VANGELKLVGDCDEGTSLVVRGRPDGKLGNAAGAAVATHLDRIRIAMSFLVGLVSENP 420  
DB 361 VANGELKLVGDCDEGTSLVVRGRPDGKLGNAAGAAVATHLDRIRIAMSFLVGLVSENP 420  
QY 421 VTYVDDATMTATSPFPEFMDMMPGLGAKIELS 450  
DB 421 VTYVDDATMTATSPFPEFMDMMPGLGAKIELS 450  
QY 447 VTYVDDSNMTATSPFPEFMDMMPGLGAKIELS 447  
DB 447 VTYVDDSNMTATSPFPEFMDMMPGLGAKIELS 447

RESULT 9  
US-09-464-099A-7  
Sequence 7, Application US/09464099A  
Patent No. US20020168680A1  
GENERAL INFORMATION:  
APPLICANT: Barry, Gerard F.  
APPLICANT: Kishore, Ganesh M.

APPLICANT: Padgett, Stephen R.  
APPLICANT: Stallings, William C.  
TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES  
FILE REFERENCE: 11899.0175.CNISO1 MOBT:175-2  
CURRENT APPLICATION NUMBER: US/09/464,099A  
CURRENT FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: US 09/137,440  
PRIOR FILING DATE: 1998-08-20  
PRIOR APPLICATION NUMBER: US 08/833,485  
PRIOR FILING DATE: 1997-04-07  
PRIOR APPLICATION NUMBER: US 08/306,063  
PRIOR FILING DATE: 1994-09-13  
PRIOR APPLICATION NUMBER: US 07/749,611  
PRIOR FILING DATE: 1991-08-28  
PRIOR APPLICATION NUMBER: US 07/576,537  
PRIOR FILING DATE: 1990-08-31  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 7  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Pseudomonas sp.  
US-09-464-099A-7

Query Match 83.1%; Score 1900.5; DB 9; Length 449;  
Best Local Similarity 82.9%; Pred. No. 1.4e-149;  
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

QY 1 MHGASSRPATARKSSGLSGTVIRIPGDKSISHSRSMFGGLASGETRITGLBSEDVINTG 60  
DB 1 MSHSASPKPATARRSALTGEIRIPGDKSISHSRSMFGGLASGETRITGLBSEDVINTG 60  
QY 61 KMOAMGAKIRKRGDWTIIDVNGGGLAPAPLDPGNATGRLTMGLVGVYDFPSTFI 120  
DB 61 RAMQAMGAKIRKRGDWTIIDVNGGGLAPAPLDPGNATGRLTMGLVGVYDFPSTFI 120  
QY 121 GDSLTKRPMGRVNLPLREMGVQVKSDEGDRPLVTLRGKPTPTITRYVPMASQVKSAN 180  
DB 121 GDSLTKRPMGRVNLPLREMGVQVKSDEGDRPLVTLRGKPTPTITRYVPMASQVKSAN 180  
QY 121 GDSLTKRPMGRVNLPLREMGVQVKSDEGDRPLVTLRGKPTPTITRYVPMASQVKSAN 180  
DB 121 GDSLTKRPMGRVNLPLREMGVQVKSDEGDRPLVTLRGKPTPTITRYVPMASQVKSAN 180  
QY 181 LLAGLNTPGITTYIEBIMTRDHEKMLQGFGANLTYETDADGVRTIRLBGRKLTQVVD 240  
DB 181 LLAGLNTPGITTYIEBIMTRDHEKMLQGFGANLTYETDADGVRTIRLBGRKLTQVVD 240  
QY 241 VEGDPESTAFPLVAALLVGSQVTLINVLNMPRTGILLTLOEMGADIEVINRLAGGED 300  
DB 241 VEGDPESTAFPLVAALLVGSQVTLINVLNMPRTGILLTLOEMGADIEVINRLAGGED 300  
QY 301 VADLRVRSSTLKGVTPEDRAPSMIDEPYLAFAAFAEGATVMNGLEELRVKESDRLSA 360  
DB 301 VADLRVRSSTLKGVTPEDRAPSMIDEPYLAFAAFAEGATVMNGLEELRVKESDRLSA 360  
QY 361 VANGELKLVGDCDEGTSLVVRGRPDGKLGNAAGAAVATHLDRIRIAMSFLVGLVSENP 420  
DB 361 VANGELKLVGDCDEGTSLVVRGRPDGKLGNAAGAAVATHLDRIRIAMSFLVGLVSENP 420  
QY 421 VTYVDDATMTATSPFPEFMDMMPGLGAKIELS 450  
DB 421 VTYVDDATMTATSPFPEFMDMMPGLGAKIELS 450  
QY 447 VTYVDDSNMTATSPFPEFMDMMPGLGAKIELS 447  
DB 447 VTYVDDSNMTATSPFPEFMDMMPGLGAKIELS 447

RESULT 10  
US-10-214-766-30  
Sequence 30, Application US/10214766  
Publication No. US20030084473A1  
GENERAL INFORMATION:  
APPLICANT: Gocal, Greg  
TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS  
FILE REFERENCE: CA1138  
CURRENT APPLICATION NUMBER: US/10/214,766  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: US 60/311,734  
PRIOR FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 53  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 30  
LENGTH: 480  
TYPE: PRF  
ORGANISM: Brucella melitensis  
NAME/KEY: misc\_feature  
LOCATION: (364)..(364)  
OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
US-10-214-766-30

Query Match 81.1%; Score 1855.5; DB 14; Length 480;  
Best Local Similarity 81.4%; Pred. No. 8.3e-146;  
Matches 364; Conservative 35; Mismatches 45; Indels 3; Gaps 1;

QY 1 MLHGASRPATARKSGLSGTVRIPGDKSISHSRPFGLASGETRITGLLEGEDVINTG 60  
DB 31 MSHSACPATARKSGLSGLTGEIRIPGDKSISHSRPFGLASGETRITGLLEGEDVINTG 90  
QY 61 KAMQAMGARIRKESGDTWIIDVGNGLLAPEAPLDFGNATGCRITMGLVGVYDPDSTFI 120  
DB 91 RAMQAMGARIRKESGDTWIIDVGNGLLAPEAPLDFGNATGCRITMGLVGVYDPDSTFI 150  
QY 121 GPASLTKRPMGVNLPLEMGVQVKSDDRLPYTLRGKPTPTTYRVPMAAQVKSAY 180  
DB 151 GPASLTKRPMGVNLPLEMGVQVKSDDRLPYTLRGKPTPTTYRVPMAAQVKSAY 210  
QY 181 LLAGLNTPGITTVIEPMTDHEKMLQSGFANLTVETDADGVRTIRLEGKLTGQV 240  
DB 211 LLAGLNTPGITTVIEPMTDHEKMLQSGFANLTVETDADGVRTIRLEGKLTGQV 270  
QY 241 VEGDPSSTAPFLVAALVPGSDVTILNVLNMPRTGILITLQEMGADIEVINPRLAGGE 300  
DB 271 VEGDPSSTAPFLVAALVPGSDVTILNVLNMPRTGILITLQEMGADIEVINPRLAGGE 330  
QY 301 VADLRVRSSTLKGTVPEDEAPSMIDEPYLAFAAFAAGATVNGLEELRVKESDRLS 360  
DB 331 VADLRVRSSTLKGTVPEDEAPSMIDEPYLAFAAFAAGATVNGLEELRVKESDRLS 390  
QY 361 VANGELKINGVDCDEGETSLVVRGPRDGKLGAGNAGAAVTHLDHRIAMSFVWGLV 420  
DB 391 VANGELKINGVDCDEGETSLVVRGPRDGKLGAGNAGAAVTHLDHRIAMSFVWGLV 447  
QY 421 VTVDATMTATSPPEFMDLMAIGAKI 447  
DB 448 VTVDATMTATSPPEFMDLMAIGAKI 474

## RESULT 11

US-10-369-493-12116  
Sequence 12116, Application US/10369493  
Publication No. US20030233675A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldman, Barry S.  
APPLICANT: Chen, Xianfeng  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
PRIOR FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 12116  
LENGTH: 452  
TYPE: PRF  
ORGANISM: Mesorhizobium loti  
US-10-369-493-12116

Query Match 77.9%; Score 1783; DB 15; Length 452;  
Best Local Similarity 77.8%; Pred. No. 8.4e-140;  
Matches 351; Conservative 33; Mismatches 63; Indels 4; Gaps 2;

QY 1 MLHGASRPATARKSGLSGTVRIPGDKSISHSRPFGLASGETRITGLLEGEDVINTG 60  
DB 1 MSHSACPATARKSGLSGLTGEIRIPGDKSISHSRPFGLASGETRITGLLEGEDVINTG 60  
QY 61 KAMQAMGARIRKESGDTWIIDVGNGLLAPEAPLDFGNATGCRITMGLVGVYDPDSTFI 120  
DB 61 KAMQAMGARIRKESGDTWIIDVGNGLLAPEAPLDFGNATGCRITMGLVGVYDPDSTFI 120  
QY 121 GPASLTKRPMGVNLPLEMGVQVKSDDRLPYTLRGKPTPTTYRVPMAAQVKSAY 179  
DB 121 GPASLTKRPMGVNLPLEMGVQVKSDDRLPYTLRGKPTPTTYRVPMAAQVKSAY 180  
QY 180 VLLAGLNTPGITTVIEPMTDHEKMLQSGFANLTVETDADGVRTIRLEGKLTGQV 239  
DB 181 VLLAGLNTPGITTVIEPMTDHEKMLQSGFANLTVETDADGVRTIRLEGKLTGQV 240  
QY 240 VEGDPSSTAPFLVAALVPGSDVTILNVLNMPRTGILITLQEMGADIEVINPRLAGGE 299  
DB 241 VEGDPSSTAPFLVAALVPGSDVTILNVLNMPRTGILITLQEMGADIEVINPRLAGGE 300  
QY 300 VADLRVRSSTLKGTVPEDEAPSMIDEPYLAFAAFAAGATVNGLEELRVKESDRLS 359  
DB 301 VADLRVRSSTLKGTVPEDEAPSMIDEPYLAFAAFAAGATVNGLEELRVKESDRLS 360  
QY 360 VANGELKINGVDCDEGETSLVVRGPRDGKLGAGNAGAAVTHLDHRIAMSFVWGLV 416  
DB 361 VANGELKINGVDCDEGETSLVVRGPRDGKLGAGNAGAAVTHLDHRIAMSFVWGLV 420  
QY 417 SENPYVDATMTATSPPEFMDLMAIGAKI 447  
DB 421 TEKPTTIDQAMTATSPPEFMDLMAIGAKI 451

## RESULT 12

US-10-369-493-20766  
Sequence 20766, Application US/10369493  
Publication No. US20030233675A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldman, Barry S.  
APPLICANT: Chen, Xianfeng  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
PRIOR FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 20766  
LENGTH: 430  
TYPE: PRF  
ORGANISM: Rhodospseudomonas palustris  
US-10-369-493-20766

Query Match 53.9%; Score 1233.5; DB 15; Length 430;  
Best Local Similarity 60.0%; Pred. No. 4.5e-94;  
Matches 259; Conservative 49; Mismatches 113; Indels 11; Gaps 5;

QY 9 PATARKSGLSGTVRIPGDKSISHSRPFGLASGETRITGLLEGEDVINTGKAMQAMGA 68  
DB 6 PATARKSGLSGTVRIPGDKSISHSRPFGLASGETRITGLLEGEDVINTGKAMQAMGA 65  
QY 69 RIRKESGDTWIIDVGNGLLAPEAPLDFGNATGCRITMGLVGVYDPDSTFI 127  
DB 66 KVERTGDCMRVHGVAGFATPEAPLDFGNATGCRITMGLVGVYDPDSTFI 125

Qy	128	RPBGRVYNPLREGVQV--VYSEGDGRLPVTLRGKPTPTTYRVPMSAQVNSAVLLAGN	186
Db	126	RPBRRILYDELMLGAKVSSBGGRLPALQGGARDPLPLTYRTPVPSAQIKSAVLLAGIS	185
Qy	187	TPGITTVEIEIMRDRHTEKMLQGFGANLIVETPADGV--RTIRLBGRGKLTQVIDVPGD	244
Db	186	APGITTIVIEAARDRHTEMLQHFGA--TIVTBEGAHGRKISLTQPELRGAPVVPVD	243
Qy	245	PSSTAEPFLVAALLVPGSDVTILNVLNMPRTGILLTQEWGADIEVINPRLAGGEDVADL	304
Db	244	PSAAFPFMAVALVPGSDIELTDVMTNPLRTGILLTRREGKASIEDSDVRGADGERMAF	303
Qy	305	RVPSSITKGYTVEDRAPSMTIDEPFLAFAAFAEGATVWNGLEBLRVKESDPLSVANG	364
Db	304	RVRGSKLKGVEVPEERAPSMIDELYLVAAFAAEGTTVWRGHEHVRKESDRLKXTAAM	363
Qy	365	LKINGVDCDGEFSLVYRGRPDGKGLGNASGAVAHHLHRIAMSLVWNGVSENPVTD	424
Db	364	LRVNGAVALVEAGDGLIVEGRGHVPG-----GGVAATHMDHRIAMSLAMGLAKDKPTVD	418
Qy	425	DATMIATSPDEF	436
Db	419	DTAFIATSPDF	430

```

1      RESULT 13
2      US-10-369-493-10476
3      ; Sequence 10476, Application US/10369493
4      ; Publication NO. US2003023675A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Cao, Yongwei
7      ; APPLICANT: Hinkle, Gregory J.
8      ; APPLICANT: Slater, Steven C.
9      ; APPLICANT: Goldman, Barry S.
10     ; APPLICANT: Chen, Xianfeng
11     ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
12     ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
13     ; FILE REFERENCE: 38-10(52052)B
14     ; CURRENT APPLICATION NUMBER: US/10/369,493
15     ; CURRENT FILING DATE: 2003-02-28
16     ; PRIOR APPLICATION NUMBER: US 60/360,039
17     ; PRIOR FILING DATE: 2002-02-21
18     ; NUMBER OF SEQ. ID NOS: 47374
19     ; SEQ. ID NO 10476
20     ; LENGTH: 432
21     ; TYPE: PRT
22     ; ORGANISM: Spingomonas aromaticivorans
23     ; US-10-369-493-10476

```

Query Match	53.04	Score 123.5	DB 15	Length 432
Best Local Similarity	59.04	Pred. No. 2.1e-82		
Matches 250	Conservative 49	Mismatches 124	Indels 1	Gaps 1
QY	18	LSGTARI PGDKS ISHRS FMFGI ASGERTITGLLEGEDEVINTGKAMQAGARIKRGD-T	76	
Db	9	LKGRIGVPGGKSI SHRSIMLGALAVGETRVTLGLEEGEDVLSTAAARNRAGATIERADQM	68	
QY	77	MIIDGVNGGLLPEARPLDFGNATGCRITMGIVGVYDPDSTIGASITKRPMGVLNP	136	
Db	69	WHYHGVGVGGLLPQDALDMGNSGSTRLLMGLVAHPITATYVGSASLSKPMGVADP	128	
QY	137	LRENGVOVKSEDDRLPVTLLRGPKTPTIITYRVPMASQVKSANVLLAGINTPGITTVIEP	196	
Db	129	LSTMGAEFTSPGGRPLTLRGISPAVPIETRRYPVASQVKSANVLLAGINTPGVTVIEP	188	
QY	197	IMTRDHEKMLQGFGANLIVETDADGVRTIRLEGKGLTQGVLDVGEDESSSTFPLVAL	256	
Db	189	IPTRDHERMLRGGALITVDVAADGARVIRVNGBAELKQDILAVGDESSSAFPPVAL	248	
QY	257	LVRGSDVTIILVMPNPRITGLITLQMGADIVINPRLAGSDVADLVRSSTLKGTVY	316	
Db	249	LVRSSDILVENVGINTPRPALFDVLIRMTGSIIELNRRVEGGEPAVDLRHSLLTGIDV	308	

[illegible]

```

RESULT 14
US-10-369-493-7814
: Sequence 7814, Application US/10369493
: Publication No. US2003023675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIORITY FILING DATE: 2003-02-28
PRIORITY APPLICATION NUMBER: US 60/360,039
PRIORITY FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7814
LENGTH: 418
TYPE: PRT
ORGANISM: Rhodobacter sphaeroides
US-10-369-493-7814

```

	Query Match	51.9%;	Score 1188.5;	DB 15;	Length 418;	
	Best Local Similarity	58.1%;	Pred. No. 2, 4e-90;			
	Matches 24/;	Conservative 52;	Mismatches 117;	Indels 9;	Gaps 4;	
Qy	18	LSGTVAIPGDKSISHSFMPGLASGETRITGLLEGEDVINTGKAMQANGAIRKEG-DT	76			
Dd	1	LKGRAEIPGGKSISHRALILIGAAVETRIITGLLEGODVLDTAKMARPAEAVIOHGPGA	60			
Qy	77	WIIDGVNGGSLAPEARLPDGNAAATCGRTIMGLGVGYDDPSFTIGDASTTKPKPMGRVLP	136			
Dd	61	WSHGCVGVGFTEPRAVIDGNSGTIVRLVMGAMATSPLTAFTGDASLRKPKMGRTYDP	120			
Qy	137	LREMGOVKSSEDRLPVTLRGEPKETPTITYRVPMASQAQVSAAVILIAGLNTPGITTVIRP	196			
Dd	121	LALFGTRAYARKKGGRILPMTLVGAADVPRVRYTPVPSPAQVKSAVILIAGLNAGQTWIER	180			
Qy	197	IMRRDHTEKKLOFGANLVTEDADQVRITRLERGKLTCGVIVDVGDDSSAFPLVAL	256			
Dd	181	EARRDSHERLRKFGEELSVETGPES-QVITTLGQPELRPYVAAPERDSSAAPFCAL	239			
Qy	257	LVEGSDDTILINLMNPTRTGLILTLIOEMADILEVINPRIAGSEDAVDLFRVRSSTLGTV	316			
Dd	240	IIVSGSELVGVCSRNPTRDGLVYTLLEMADIAFENEREDEGPVADLKVRSALKGVET	299			
Qy	317	PEBRASPMDIERYILAAVAFAEGATVWNGLEBLRKESDRISAANGIKLVGDCDEE	376			
Dd	300	PPRAPBMIDEYIILSVAAFAEGLITMKGVELRKESDRIDANAARGLEACGVNIEBE	359			
Qy	377	TSLVGRPDGKGIAGNA-SGAAVATHLDRIIRIMSFLVMGLVENPPTYVDATAIMATSP	435			
Dd	360	DTLIIV-----GMGRVPGGATCATHLDRIRIMSFVLGMABAPVTDGDSPIATSPFA	413			
Qy	436	FNDLM 440				
Dd	414	FIDL 418				



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 20, 2005, 15:18:11 ; Search time 44 Seconds  
(without alignments)  
771.939 Million cell updates/sec

Title: US-10-622-201-70  
Perfect score: 2288  
Sequence: 1 MLHGASRRPARKSSGLSG.....FMDLMAGLAKITLSDTRAA 455

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/6CTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2282	99.7	455	1	US-08-476-008-3
2	2282	99.7	455	1	US-08-306-063-3
3	2282	99.7	455	1	US-08-833-485-3
4	2282	99.7	455	5	US-09-137-440-3
5	2282	99.7	455	5	PCT-US91-06148A-3
6	1900.5	83.1	449	1	US-08-476-008-5
7	1900.5	83.1	449	1	US-08-306-063-5
8	1900.5	83.1	449	1	US-08-306-063-7
9	1900.5	83.1	449	1	US-08-306-063-7
10	1900.5	83.1	449	1	US-08-833-485-5
11	1900.5	83.1	449	1	US-08-833-485-7
12	1900.5	83.1	449	3	US-09-137-440-5
13	1900.5	83.1	449	3	US-09-137-440-7
14	1900.5	83.1	449	5	PCT-US91-06148A-5
15	1900.5	83.1	449	5	PCT-US91-06148A-7
16	1092	47.7	220	3	US-09-011-151-13
17	989.5	43.2	782	4	US-09-252-991A-21554
18	961.5	42.0	758	4	US-09-252-991A-21554
19	902.5	39.4	773	4	US-09-540-236-3590
20	867.5	37.9	447	1	US-08-476-008-67
21	867.5	37.9	447	1	US-08-306-063-67
22	867.5	37.9	447	1	US-08-833-485-67
23	867.5	37.9	447	3	US-09-137-440-67
24	866	37.4	177	3	US-09-011-151-15
25	856	37.4	431	4	US-09-107-532A-7163
26	807.5	35.3	459	4	US-09-107-433-4297
27	806	35.2	443	1	US-08-476-008-69

28	806	35.2	443	1	US-08-306-063-69	Sequence 69, Appl
29	806	35.2	443	1	US-08-833-485-69	Sequence 69, Appl
30	806	35.2	443	1	US-09-137-440-69	Sequence 69, Appl
31	805.5	35.2	427	4	US-09-583-110-3546	Sequence 3546, Ap
32	803.5	35.1	427	3	US-09-325-881-2	Sequence 2, Appl
33	798.5	34.9	427	2	US-08-896-345-2	Sequence 2, Appl
34	798.5	34.9	427	3	US-08-476-008-42	Sequence 42, Appl
35	785	34.3	428	1	US-08-306-063-42	Sequence 42, Appl
36	785	34.3	428	1	US-08-833-485-42	Sequence 42, Appl
37	785	34.3	428	3	US-09-137-440-42	Sequence 42, Appl
38	785	34.3	428	3	US-09-134-000C-4980	Sequence 4980, Ap
39	781.5	34.2	430	4	US-08-896-345-4	Sequence 4, Appl
40	704.5	30.8	415	2	US-09-226-091-4	Sequence 4, Appl
41	704.5	30.8	415	3	US-09-325-881-4	Sequence 4, Appl
42	704.5	30.8	415	3	US-09-134-001C-3223	Sequence 3223, Ap
43	623	27.2	436	3	US-08-476-008-44	Sequence 44, Appl
44	577	25.2	430	1	US-08-306-063-44	Sequence 44, Appl
45	577	25.2	430	1	US-08-306-063-44	Sequence 44, Appl

## ALIGNMENTS

RESULT 1  
US-08-476-008-3  
Sequence 3, Application US/08476008  
Patent No. 5627061  
GENERAL INFORMATION:  
APPLICANT: Barry, Gerard F.  
APPLICANT: Kishore, Ganesh M.  
APPLICANT: Padgett, Stephen R.  
APPLICANT: Stallings, William C.  
TITLE OF INVENTION: Glycosylase Tolerant  
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF  
STREET: 700 Chesterfield Village Parkway  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,008  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,063  
FILING DATE: 13-SEP-1994  
APPLICATION NUMBER: US 07/749,611  
FILING DATE: 28-AUG-1991  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/576,537  
FILING DATE: 31-AUG-1990  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoerner Jr., Dennis R.  
REGISTRATION NUMBER: 30,914  
REFERENCE/DOCKET NUMBER: 38-21(10660)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)537-6099  
TELEFAX: (314)537-6047  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

```

MOLECULE TYPE: protein
US-08-476-008-3
Query Match      99.7%; Score 2282; DB 1; Length 455;
Best Local Similarity 99.8%; Pred. No. 1.9e-201;
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHHGSSRPATRKSSGSGTVRIIPGDKSISHSRPFMGGLASGETRITGLLEGEDVINTG 60
DB 1 MSHGASSRPATRKSSGSGTVRIIPGDKSISHSRPFMGGLASGETRITGLLEGEDVINTG 60
QY 61 KAMQAMGARIRKRGDPTWIIDGVNGGLAPAPLDFGNAATGCRITMGLVGYDFDSTFI 120
DB 61 KAMQAMGARIRKRGDPTWIIDGVNGGLAPAPLDFGNAATGCRITMGLVGYDFDSTFI 120
QY 121 GPASLTKRPMGRVNLPLREMGVQVKSDEGDRLPVTLRGPKPTPTTYRVPMASQVKSANV 180
DB 121 GPASLTKRPMGRVNLPLREMGVQVKSDEGDRLPVTLRGPKPTPTTYRVPMASQVKSANV 180
QY 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGKLTGOVID 240
DB 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGKLTGOVID 240
QY 241 VPDPSSSTAFPLVAALLVPGSDVTILNVMNPTRTGLILTLQEMGADIEVINPRLAGGED 300
DB 241 VPDPSSSTAFPLVAALLVPGSDVTILNVMNPTRTGLILTLQEMGADIEVINPRLAGGED 300
QY 301 VADLRVRSSTLKGTVPEPDRAPSMIDEYPIILAVAAFAEGATVMNGLEELRYKESDRLSA 360
DB 301 VADLRVRSSTLKGTVPEPDRAPSMIDEYPIILAVAAFAEGATVMNGLEELRYKESDRLSA 360
QY 361 VANGKLKNGVDCDEBETSLVVRGPRDGKGLGNASGAAVAATHLDRIRAMSFVLMGLVSENP 420
DB 361 VANGKLKNGVDCDEBETSLVVRGPRDGKGLGNASGAAVAATHLDRIRAMSFVLMGLVSENP 420
QY 421 VTVDATMIATSPPEFMDLMAGLGAKEIELSDTKAA 455
DB 421 VTVDATMIATSPPEFMDLMAGLGAKEIELSDTKAA 455

RESULT 2
US-08-306-063-3
Sequence 3, Application US/08306063
Patent No. 5633435
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glycosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,063
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

```

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APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-306-063-3
Query Match      99.7%; Score 2282; DB 1; Length 455;
Best Local Similarity 99.8%; Pred. No. 1.9e-201;
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHHGSSRPATRKSSGSGTVRIIPGDKSISHSRPFMGGLASGETRITGLLEGEDVINTG 60
DB 1 MSHGASSRPATRKSSGSGTVRIIPGDKSISHSRPFMGGLASGETRITGLLEGEDVINTG 60
QY 61 KAMQAMGARIRKRGDPTWIIDGVNGGLAPAPLDFGNAATGCRITMGLVGYDFDSTFI 120
DB 61 KAMQAMGARIRKRGDPTWIIDGVNGGLAPAPLDFGNAATGCRITMGLVGYDFDSTFI 120
QY 121 GPASLTKRPMGRVNLPLREMGVQVKSDEGDRLPVTLRGPKPTPTTYRVPMASQVKSANV 180
DB 121 GPASLTKRPMGRVNLPLREMGVQVKSDEGDRLPVTLRGPKPTPTTYRVPMASQVKSANV 180
QY 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGKLTGOVID 240
DB 181 LLAGINTPGITTVIEPIIMTRDHTKMLQGFGANLTVETDADGVRTIRLEGKLTGOVID 240
QY 241 VPDPSSSTAFPLVAALLVPGSDVTILNVMNPTRTGLILTLQEMGADIEVINPRLAGGED 300
DB 241 VPDPSSSTAFPLVAALLVPGSDVTILNVMNPTRTGLILTLQEMGADIEVINPRLAGGED 300
QY 301 VADLRVRSSTLKGTVPEPDRAPSMIDEYPIILAVAAFAEGATVMNGLEELRYKESDRLSA 360
DB 301 VADLRVRSSTLKGTVPEPDRAPSMIDEYPIILAVAAFAEGATVMNGLEELRYKESDRLSA 360
QY 361 VANGKLKNGVDCDEBETSLVVRGPRDGKGLGNASGAAVAATHLDRIRAMSFVLMGLVSENP 420
DB 361 VANGKLKNGVDCDEBETSLVVRGPRDGKGLGNASGAAVAATHLDRIRAMSFVLMGLVSENP 420
QY 421 VTVDATMIATSPPEFMDLMAGLGAKEIELSDTKAA 455
DB 421 VTVDATMIATSPPEFMDLMAGLGAKEIELSDTKAA 455

RESULT 3
US-08-833-485-3
Sequence 3, Application US/08833485
Patent No. 5804425
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glycosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA

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ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,485  
FILING DATE: 07-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,063  
FILING DATE: 13-SEP-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,611  
FILING DATE: 28-AUG-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/576,537  
FILING DATE: 31-AUG-1990  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoerner Jr., Dennis R.  
REGISTRATION NUMBER: 30,914  
REFERENCE/DOCKET NUMBER: 38-21(15117)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)737-6099  
TELEFAX: (314)737-6047  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-833-485-3

Query Match  
Best Local Similarity 99.7%; Score 2282; DB 1; Length 455;  
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MLHGASSRPARARKSSGLSGTVRIPEGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
1 MSHGASSRPARARKSSGLSGTVRIPEGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
61 KAMQAMGARIKREGDWTIIDGVNGGLAPAPLDFGNATGCRITMGVGYDFDSTFI 120  
61 KAMQAMGARIKREGDWTIIDGVNGGLAPAPLDFGNATGCRITMGVGYDFDSTFI 120  
121 GNASLTKRPMGRVLPNLRMGVQVKSDDRLPVTLRGKPTPTPIYRVPMASQVKSAY 180  
121 GNASLTKRPMGRVLPNLRMGVQVKSDDRLPVTLRGKPTPTPIYRVPMASQVKSAY 180  
181 LLAGLNTPGITTVIEBIMTRDHTKMLQGFGANLIVETDADGVRTIRLEGKLTGQVID 240  
181 LLAGLNTPGITTVIEBIMTRDHTKMLQGFGANLIVETDADGVRTIRLEGKLTGQVID 240  
241 VPQDPSSTAFPLVAAALVPGSDVTIINVMPTRTGLIITLQMGADIEVINRLAGSD 300  
241 VPQDPSSTAFPLVAAALVPGSDVTIINVMPTRTGLIITLQMGADIEVINRLAGSD 300  
301 VADLRVRSSTLKGVTVPEDRAPSMDIEYPLVAAAPAGATVMNGLLEELRVKESDRLA 360  
301 VADLRVRSSTLKGVTVPEDRAPSMDIEYPLVAAAPAGATVMNGLLEELRVKESDRLA 360  
361 VANGKLINGVDCDEGTSLVVRGRPDGKIGNAGAAVATHLDRITAMSEFLVGLVSENP 420  
361 VANGKLINGVDCDEGTSLVVRGRPDGKIGNAGAAVATHLDRITAMSEFLVGLVSENP 420  
421 VTYDDATMTATSPFPMDLMAIGAKIEISDPTKAA 455  
421 VTYDDATMTATSPFPMDLMAIGAKIEISDPTKAA 455  
421 VTVDATMTATSPFPMDLMAIGAKIEISDPTKAA 455

RESULT 4  
US-09-137-440-3  
Sequence 3, Application US/09137440  
Patent No. 6248876  
GENERAL INFORMATION:  
APPLICANT: Barry, Gerard F.  
APPLICANT: Kishore, Ganesh M.  
APPLICANT: Padgett, Stephen R.  
APPLICANT: Stallings, William C.  
TITLE OF INVENTION: Glycosate Tolerant  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B44F  
STREET: 700 Chesterfield Village Parkway  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/137,440  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/833,485  
FILING DATE: 07-APR-1997  
APPLICATION NUMBER: US 08/306,063  
FILING DATE: 13-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,611  
FILING DATE: 28-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/576,537  
FILING DATE: 31-AUG-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoerner Jr., Dennis R.  
REGISTRATION NUMBER: 30,914  
REFERENCE/DOCKET NUMBER: 38-21(15117)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)737-6099  
TELEFAX: (314)737-6047  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-137-440-3

Query Match  
Best Local Similarity 99.7%; Score 2282; DB 3; Length 455;  
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MLHGASSRPARARKSSGLSGTVRIPEGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
1 MSHGASSRPARARKSSGLSGTVRIPEGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
61 KAMQAMGARIKREGDWTIIDGVNGGLAPAPLDFGNATGCRITMGVGYDFDSTFI 120  
61 KAMQAMGARIKREGDWTIIDGVNGGLAPAPLDFGNATGCRITMGVGYDFDSTFI 120  
121 GNASLTKRPMGRVLPNLRMGVQVKSDDRLPVTLRGKPTPTPIYRVPMASQVKSAY 180  
121 GNASLTKRPMGRVLPNLRMGVQVKSDDRLPVTLRGKPTPTPIYRVPMASQVKSAY 180  
181 LLAGLNTPGITTVIEBIMTRDHTKMLQGFGANLIVETDADGVRTIRLEGKLTGQVID 240  
181 LLAGLNTPGITTVIEBIMTRDHTKMLQGFGANLIVETDADGVRTIRLEGKLTGQVID 240

Db 181 LLAGNTGCTTIVIPITRDTHEKMLQGFANLTVETDADGVRTIRLEGKLTGQVID 240  
Qy 241 VPGDSSSTAPFLVALLVPGSDVTILNLVNMPTRTGLITLQEMGADIEVINPRLAGGED 300  
Db 241 VPGDSSSTAPFLVALLVPGSDVTILNLVNMPTRTGLITLQEMGADIEVINPRLAGGED 300  
Qy 301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIILAVAAAFEGATVNMGLEELRVKESDRLSA 360  
Db 301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIILAVAAAFEGATVNMGLEELRVKESDRLSA 360  
Qy 361 VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAATAVTHLDRIRIAMSFLVMGLVSENP 420  
Db 361 VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAATAVTHLDRIRIAMSFLVMGLVSENP 420  
Qy 421 VTVDATMIATSPPEFMDLMAGLGAKIELSDTKAA 455  
Db 421 VTVDATMIATSPPEFMDLMAGLGAKIELSDTKAA 455

RESULT 5  
PCT-US91-06148A-3  
Sequence 3, Application PC/TUS9106148A  
GENERAL INFORMATION:  
APPLICANT: Barry, Gerard F.  
APPLICANT: Kishore, Ganesh M.  
APPLICANT: Padgett, Stephen R.  
TITLE OF INVENTION: Glyphosate Tolerant  
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF  
STREET: 700 Chesterfield Village Parkway  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/06148A  
FILING DATE: 19910828  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,611  
FILING DATE: 28-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/576,537  
FILING DATE: 31-AUG-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoerner Jr., Dennis R.  
REGISTRATION NUMBER: 30,914  
REFERENCE/DOCKET NUMBER: 38-21(10535)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)537-6047  
TELEFAX: (314)537-6047  
INFORMATION FOR SEO ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US91-06148A-3

Query Match 99.7%; Score 2282; DB 5; Length 455;  
Best Local Similarity 99.8%; Pred. No. 1.9e-201;  
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLHGASSPATARKSSGLSGTIRIPGDKSISHSRPFMGSLAGSERITGLGEGDVINTG 60  
Db 1 MSHGASSPATARKSSGLSGTIRIPGDKSISHSRPFMGSLAGSERITGLGEGDVINTG 60

Qy 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLDFGNAATGCRITWGLVGVYDFDSTFI 120  
Db 61 KAMQAMGARIRKEGDTWIIDGVNGGLAPAPLDFGNAATGCRITWGLVGVYDFDSTFI 120  
Qy 121 GDASTTRKPMGRVNLNPLEMVOVKSEEDGRLPTLRGPKPTPTTYVPMASQVKSAY 180  
Db 121 GDASTTRKPMGRVNLNPLEMVOVKSEEDGRLPTLRGPKPTPTTYVPMASQVKSAY 180  
Qy 181 LLAGNTGCTTIVIPITRDTHEKMLQGFANLTVETDADGVRTIRLEGKLTGQVID 240  
Db 181 LLAGNTGCTTIVIPITRDTHEKMLQGFANLTVETDADGVRTIRLEGKLTGQVID 240  
Qy 241 VPGDSSSTAPFLVALLVPGSDVTILNLVNMPTRTGLITLQEMGADIEVINPRLAGGED 300  
Db 241 VPGDSSSTAPFLVALLVPGSDVTILNLVNMPTRTGLITLQEMGADIEVINPRLAGGED 300  
Qy 301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIILAVAAAFEGATVNMGLEELRVKESDRLSA 360  
Db 301 VADLRVRSSTLKGVTVPEDRAPSMIDEYPIILAVAAAFEGATVNMGLEELRVKESDRLSA 360  
Qy 361 VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAATAVTHLDRIRIAMSFLVMGLVSENP 420  
Db 361 VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNASGAATAVTHLDRIRIAMSFLVMGLVSENP 420  
Qy 421 VTVDATMIATSPPEFMDLMAGLGAKIELSDTKAA 455  
Db 421 VTVDATMIATSPPEFMDLMAGLGAKIELSDTKAA 455

RESULT 6  
US-08-476-008-5  
Sequence 5, Application US/08476008  
Patent No. 5627061  
GENERAL INFORMATION:  
APPLICANT: Barry, Gerard F.  
APPLICANT: Kishore, Ganesh M.  
APPLICANT: Padgett, Stephen R.  
APPLICANT: Stallings, William C.  
TITLE OF INVENTION: Glyphosate Tolerant  
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF  
STREET: 700 Chesterfield Village Parkway  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08476,008  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,063  
FILING DATE: 13-SEP-1994  
APPLICATION NUMBER: US 07/749,611  
FILING DATE: 28-AUG-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/576,537  
FILING DATE: 31-AUG-1990  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoerner Jr., Dennis R.  
REGISTRATION NUMBER: 30,914  
REFERENCE/DOCKET NUMBER: 38-21(10660)A  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (314)537-6099  
 TELEFAX: (314)537-6047  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 449 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-476-008-5

Query Match 83.1%; Score 1900.5; DB 1; Length 449;  
 Best Local Similarity 82.9%; Pred. No. 2,4e-166;  
 Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

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QY 1 MLHGASSRPARATARKSSGSGTVRIIPGDKSISHRSEFMFGLASGETRITGLGEGDIYNTG 60
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Db 1 MHSASPKRATARRBALTGEIRIPGDKSISHRSEFMFGLASGETRITGLGEGDIYNTG 60
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 KAMQAMGARIRKRGDTWIIDVGNGLLAPEAPLDFGNATGCRITMGLVGYVDFDSTPI 120
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RAMQAMGAKIRKRGDVIININGVNGCLLPALADFGNAGTGARLTMGVGYVDMKTSPI 120
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 GPASLTKRMGVNLPRLRMGVQVKSDEGDLPTLRGKRTPTPTTYRVPMAAQYKSAV 180
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GPASLTKRMGVNLPRLRMGVQVKSDEGDLPTLRGKRTPTPTTYRVPMAAQYKSAV 180
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 LLAGLNTPGITTVIPIRMDHTEKMLQGFANLTVETDADGVRTIRLEGRGLTGOVID 240
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 LLAGLNTPGITTVIPIRMDHTEKMLQGFADLIVETDKDGRHRTIRIGQGLVGOITD 240
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 VPGDPSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLITLQEMGADIEVINPRLAGSD 300
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 VPGDPSSTAFPLVAALLVPGSDVTIRNVLMNPTRTGLITLQEMGADIEVINARLAGSD 300
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 301 VADLRVRSSTLKGTVPEEDRAPSMIDEYPIILAVAAAPAGATVANGLEELRYKESDRLSA 360
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 VADLRVRSSTLKGTVVPPERAPSMIDEYPIILAAAFAGEETVMGDLRLRYKESDRLAA 360
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 361 VANGKLINGVDDEGETSLVVRGPRDGKLGNAAGAAVATHLDRIRMSFLVWGLVSENP 420
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 361 VARGLEANGVDCTEGGMSLTVRGRPDGKLG--GGTAVATHLDRIRMSFLVWGLAERXP 417
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 421 VTVDATMIATSPPEFMDLMAIGAKIELS 450
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 418 VTVDSDNMIATSPPEFMDMPGLGAKIELS 447
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RESULT 7  
 US-08-476-008-7  
 ; Sequence 7, Application us/08476008  
 ; Patent No. 5627061  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Barry, Gerard F.  
 ; APPLICANT: Kishore, Ganesh M.  
 ; APPLICANT: Padgett, Stephen R.  
 ; APPLICANT: Stallings, William C.  
 ; TITLE OF INVENTION: Glycosylate Tolerant  
 ; TITLE OF SEQUENCES: 5-Ethoxytryptophan-3-Phosphate Synthases  
 ; NUMBER OF SEQUENCES: 69  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B4F  
 ; STREET: 700 Chesterfield Village Parkway  
 ; CITY: St. Louis  
 ; STATE: Missouri  
 ; COUNTRY: USA  
 ; ZIP: 63198  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/476,008

FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/306,063  
 FILING DATE: 13-SEP-1994  
 APPLICATION NUMBER: US 07/749,611  
 FILING DATE: 28-AUG-1991  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/576,537  
 FILING DATE: 31-AUG-1990  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hoerner Jr., Dennis R.  
 REGISTRATION NUMBER: 30,914  
 REFERENCE/DOCKET NUMBER: 38-21(10660)A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (314)537-6099  
 TELEFAX: (314)537-6047  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 449 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-476-008-7

Query Match 83.1%; Score 1900.5; DB 1; Length 449;  
 Best Local Similarity 82.9%; Pred. No. 2,4e-166;  
 Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

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QY 1 MLHGASSRPARATARKSSGSGTVRIIPGDKSISHRSEFMFGLASGETRITGLGEGDIYNTG 60
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MHSASPKRATARRBALTGEIRIPGDKSISHRSEFMFGLASGETRITGLGEGDIYNTG 60
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 KAMQAMGARIRKRGDTWIIDVGNGLLAPEAPLDFGNATGCRITMGLVGYVDFDSTPI 120
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RAMQAMGAKIRKRGDVIININGVNGCLLPALADFGNAGTGARLTMGVGYVDMKTSPI 120
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 GPASLTKRMGVNLPRLRMGVQVKSDEGDLPTLRGKRTPTPTTYRVPMAAQYKSAV 180
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GPASLTKRMGVNLPRLRMGVQVKSDEGDLPTLRGKRTPTPTTYRVPMAAQYKSAV 180
   |||:||||:~|:~|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 LLAGLNTPGITTVIPIRMDHTEKMLQGFANLTVETDADGVRTIRLEGRGLTGOVID 240
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 LLAGLNTPGITTVIPIRMDHTEKMLQGFADLIVETDKDGRHRTIRIGQGLVGOITD 240
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 VPGDPSSTAFPLVAALLVPGSDVTILNVLMNPTRTGLITLQEMGADIEVINPRLAGSD 300
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 VPGDPSSTAFPLVAALLVPGSDVTIRNVLMNPTRTGLITLQEMGADIEVINARLAGSD 300
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 301 VADLRVRSSTLKGTVPEEDRAPSMIDEYPIILAVAAAPAGATVANGLEELRYKESDRLSA 360
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 VADLRVRSSTLKGTVVPPERAPSMIDEYPIILAAAFAGEETVMGDLRLRYKESDRLAA 360
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 361 VANGKLINGVDDEGETSLVVRGPRDGKLGNAAGAAVATHLDRIRMSFLVWGLVSENP 420
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 361 VARGLEANGVDCTEGGMSLTVRGRPDGKLG--GGTAVATHLDRIRMSFLVWGLAERXP 417
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 421 VTVDATMIATSPPEFMDLMAIGAKIELS 450
   |||:||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 418 VTVDSDNMIATSPPEFMDMPGLGAKIELS 447
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RESULT 8  
 US-08-306-063-5  
 ; Sequence 5, Application us/08306063  
 ; Patent No. 5633435  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Barry, Gerard F.  
 ; APPLICANT: Kishore, Ganesh M.  
 ; APPLICANT: Padgett, Stephen R.  
 ; APPLICANT: Stallings, William C.

```

/ TITLE OF INVENTION: Glycosate Tolerant
/ TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
/ NUMBER OF SEQUENCES: 69
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
/ STREET: 700 Chesterfield Village Parkway
/ CITY: St. Louis
/ STATE: Missouri
/ COUNTRY: USA
/ ZIP: 63198
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/306,063
/ FILING DATE: 13-SEP-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/749,611
/ FILING DATE: 28-AUG-1991
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/576,537
/ FILING DATE: 31-AUG-1990
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hoerner Jr., Dennis R.
/ REGISTRATION NUMBER: 30,914
/ REFERENCE/DOCKET NUMBER: 38-21(10660)A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (314)537-6047
/ TELEFAX: (314)537-6099
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 449 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-306-063-5

Query Match      83.1%; Score 1900.5; DB 1; Length 449;
Best Local Similarity 82.9%; Pred. No. 2.4e-166;
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

QY 1 MLHGASRPATARKSSGSGTIRIPGDKSISHSRSMFGGLASGETRITGLLEGEDVINTG 60
DB 1 MSHSASPRKATARRSEALTGEIRIPGDKSISHSRSMFGGLASGETRITGLLEGEDVINTG 60
QY 61 KAMQAMGARIRKREGDTWIIDGVNGGLAPAPLDFGNAAATGCRITMGLVGYDSDSTFI 120
DB 61 RAMQAMGARIRKREGDWTIINGVNGGLQPEALDFGNAGTARLTMGLVGYDMDKTSFI 120
QY 121 GPASLTKRPMGVNLPLEMGVQVSEDDRLPVTLRGKPTPTITRYRPMASAOVKSAY 180
DB 121 GPASLSKRWGVNLPLEMGVQVEADDRMPVLTIGKRIANPITTYRPMASAOVKSAY 180
QY 181 ILAAGLNTPGITTVIPIRMDHTEKMLQGFANLTVETDADGVRTIRLGRGLTGOVTD 240
DB 181 ILAAGLNTPGVTVIPIRMDHTEKMLQGFADLVETKDGVRHIRTIGQGLVGOVTTD 240
QY 241 VEGDPSSTAPLVAALLVPGSDVTIILVLMNPTRTGLILTLQEMGADIEVINPRLAAGSD 300
DB 241 VEGDPSSTAPLVAALLVPGSDVTIRNVLMNPTRTGLILTLQEMGADIEVLNARLAGSD 300
QY 301 VADLVRSTTLGVTVYPEDRAPSMDIETITLAVAAAPAGATVWNGLEELRYKESDRLSA 360
DB 301 VADLVRASKTLGVTVYPPERAPSMDIETIYVLAIAAFAGETVMDGLDELRYKESDRLSA 360
QY 361 VANGKLINGVDDEGFTSLVVRGRPDGKLGNAAGAAVATHLDHRIAMSFLVWGLVSENP 420
DB 361 VARGLEANGVDCTEGEMSLTVRGRPDGKLG--GGTVATHLDHRIAMSLVWGLAAERK 417

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QY 421 VTVDATWIAISFPFMDLMAGLAKIILS 450
DB 418 VTVDSDNMIATISFPFMDMPLGAKIILS 447

RESULT 9
US-08-306-063-7
/ Sequence 7, Application US/08306063
/ Patent No. 5633435
/ GENERAL INFORMATION:
/ APPLICANT: Barry, Gerard F.
/ APPLICANT: Kishore, Ganesh M.
/ APPLICANT: Padgett, Stephen R.
/ APPLICANT: Stallings, William C.
/ TITLE OF INVENTION: Glycosate Tolerant
/ TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
/ NUMBER OF SEQUENCES: 69
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
/ STREET: 700 Chesterfield Village Parkway
/ CITY: St. Louis
/ STATE: Missouri
/ COUNTRY: USA
/ ZIP: 63198
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/306,063
/ FILING DATE: 13-SEP-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/749,611
/ FILING DATE: 28-AUG-1991
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/576,537
/ FILING DATE: 31-AUG-1990
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hoerner Jr., Dennis R.
/ REGISTRATION NUMBER: 30,914
/ REFERENCE/DOCKET NUMBER: 38-21(10660)A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (314)537-6099
/ TELEFAX: (314)537-6047
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 449 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-306-063-7

Query Match      83.1%; Score 1900.5; DB 1; Length 449;
Best Local Similarity 82.9%; Pred. No. 2.4e-166;
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

QY 1 MLHGASRPATARKSSGSGTIRIPGDKSISHSRSMFGGLASGETRITGLLEGEDVINTG 60
DB 1 MSHSASPRKATARRSEALTGEIRIPGDKSISHSRSMFGGLASGETRITGLLEGEDVINTG 60
QY 61 KAMQAMGARIRKREGDTWIIDGVNGGLAPAPLDFGNAAATGCRITMGLVGYDSDSTFI 120
DB 61 RAMQAMGARIRKREGDWTIINGVNGGLQPEALDFGNAGTARLTMGLVGYDMDKTSFI 120
QY 121 GPASLTKRPMGVNLPLEMGVQVSEDDRLPVTLRGKPTPTITRYRPMASAOVKSAY 180
DB 121 GPASLSKRWGVNLPLEMGVQVEADDRMPVLTIGKRIANPITTYRPMASAOVKSAY 180

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QY 181 LLAGNTPGITTVIEPIIMTRDHTERKLOFGANLTVETDADGVRTIRLEGKLTGVQVID 240
Db 181 LLAGNTPGITTVIEPIIMTRDHTERKLOFGADLTVEITDKDGVRIIRITGOGKLVGQTTID 240
QY 241 VGDPSSTAFLVVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGGED 300
Db 241 VGDPSSTAFLVVAALLVPGSDVTIRNVMNPTRTGLITLQEMGADIEVINARLAGGED 300
QY 301 VADLRVRSSTLKGTVVPEDRAPSMIDEYPIILVAAAFAGATVMGLLEELRVKESDRLSA 360
Db 301 VADLRVRSSTLKGTVVPEDRAPSMIDEYPIILVAAAFAGATVMGLLEELRVKESDRLSA 360
QY 361 VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNAAGAAVATHDHRIRAMSLVMGLVSENP 420
Db 361 VARGLEANGVDCDEGETSLVVRGRPDGKGLG---GGTVAATHDHRIRAMSLVMGLVLAERK 417
QY 421 VTVDATMIATSPPEFMDLMAGLAKIELS 450
Db 418 VTVDSDMIATSPPEFMDLMAGLAKIELS 447

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RESULT 10
US-08-833-485-5
; Sequence 5, Application US/08833485
; Patent No. 5804425
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: Glyphosate Tolerant
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,485
; FILING DATE: 07-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,063
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,611
; FILING DATE: 28-AUG-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/576,537
; FILING DATE: 31-AUG-1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6099
; TELEFAX: (314)737-6047
; INFORMATION FOR SEO ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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MOLECULE TYPE: protein  
US-08-833-485-5

Query Match 83.1%; Score 1900.5; DB 1; Length 449;  
Best Local Similarity 82.9%; Pred No. 2.4e-166;  
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

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QY 1 MHGASSRPATARKSSGLSGTVRIIPDKSISHSRSMFGGLASGETRITGLGEGDVINTG 60
Db 1 MSHSASPRATARRSEALTGRIIRIPGDKSISHSRSMFGGLASGETRITGLGEGDVINTG 60
QY 61 KAMQAMGARIRKESGTWIIDGVNGGLAPAPLDFGNAATGCRLTMLGVYDPTSTI 120
Db 61 RAMQAMGARIRKESGTWIIINGVNGCLLPAPALDFGNAATGCRLTMLGVYDPTSTI 120
QY 121 GDASLTKRPMGRVNLPLREMGVQVSEDDRLPVTLRGKPTPTITVRPMASAOVKSAY 180
Db 121 GDASLTKRPMGRVNLPLREMGVQVSEADGRNPLTLIGKTNPTITVRPMASAOVKSAY 180
QY 181 LLAGNTPGITTVIEPIIMTRDHTERKLOFGANLTVETDADGVRTIRLEGKLTGVQVID 240
Db 181 LLAGNTPGITTVIEPIIMTRDHTERKLOFGADLTVEITDKDGVRIIRITGOGKLVGQTTID 240
QY 241 VGDPSSTAFLVVAALLVPGSDVTILNVMNPTRTGLITLQEMGADIEVINPRLAGGED 300
Db 241 VGDPSSTAFLVVAALLVPGSDVTIRNVMNPTRTGLITLQEMGADIEVINARLAGGED 300
QY 301 VADLRVRSSTLKGTVVPEDRAPSMIDEYPIILVAAAFAGATVMGLLEELRVKESDRLSA 360
Db 301 VADLRVRSSTLKGTVVPEDRAPSMIDEYPIILVAAAFAGATVMGLLEELRVKESDRLSA 360
QY 361 VANGKLKNGVDCDEGETSLVVRGRPDGKGLGNAAGAAVATHDHRIRAMSLVMGLVSENP 420
Db 361 VARGLEANGVDCDEGETSLVVRGRPDGKGLG---GGTVAATHDHRIRAMSLVMGLVLAERK 417
QY 421 VTVDATMIATSPPEFMDLMAGLAKIELS 450
Db 418 VTVDSDMIATSPPEFMDLMAGLAKIELS 447

```

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RESULT 11
US-08-833-485-7
; Sequence 7, Application US/08833485
; Patent No. 5804425
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: Glyphosate Tolerant
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,485
; FILING DATE: 07-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,063
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 07/749,611  
FILING DATE: 28-AUG-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/576,537  
FILING DATE: 31-AUG-1990  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoerner Jr., Dennis R.  
REGISTRATION NUMBER: 30,914  
REFERENCE/DOCKET NUMBER: 38-21(15117)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)737-6099  
TELEFAX: (314)737-6047  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 449 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-833-485-7

Query Match 83.1%; Score 1900.5; DB 1; Length 449;  
Best Local Similarity 82.9%; Pred. No. 2.4e-166;  
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

QY 1 MLGASSRPATARKSSGLSGTVRIIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
DB 1 MSHSASPRTARRESEALTEGIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
QY 61 KAMQMGARIRKEGDTWIIDGVNGGLAPAPLDFGNAATGCRITMGLVGYDDSTFI 120  
DB 61 RAMQMGAKIRKEGDTWIIINGVNGCLQPEALDFGNAAGTARITMGLVGYDDSTFI 120  
QY 121 GPASLTGKPMGRVNLPLREMGVQVSEDDRLPVTLRGPKTPTPTTYRVPMASAOVKSAY 180  
DB 121 GPASLTGKPMGRVNLPLREMGVQVSEDDRLPVTLRGPKTPTPTTYRVPMASAOVKSAY 180  
QY 181 LLAGINTPGITTVIEPIIMTRDHTERKMLQGFANLIVETDADGVRTIRLEGRKLTGOVID 240  
DB 181 LLAGINTPGITTVIEPIIMTRDHTERKMLQGFANLIVETDADGVRTIRLEGRKLTGOVID 240  
QY 241 VPGDSSSTAFLVLAALVLEGSVITIRNVLMPRTGILITLOEMGADIEVLNARLAGGED 300  
DB 241 VPGDSSSTAFLVLAALVLEGSVITIRNVLMPRTGILITLOEMGADIEVLNARLAGGED 300  
QY 301 VADLVRSSLTGKGVVPPEDRAPSMIDEPILAVAAFAEGATVMNGLEELRYKESDRISA 360  
DB 301 VADLVRSSLTGKGVVPPEDRAPSMIDEPILAVAAFAEGATVMNGLEELRYKESDRISA 360  
QY 361 VANGKLINGVDCDEGETSLVVRGPDGKGLGNASGAATAVTHLDHRIAMSLVMGLVSENP 420  
DB 361 VANGKLINGVDCDEGETSLVVRGPDGKGLGNASGAATAVTHLDHRIAMSLVMGLVSENP 420  
QY 421 VTVDATMTATSPPEFMDLMAGLGAKIELS 450  
DB 421 VTVDATMTATSPPEFMDLMAGLGAKIELS 450  
QY 448 VTVDSSNMTATSPPEFMDMPLGAKIELS 447  
DB 448 VTVDSSNMTATSPPEFMDMPLGAKIELS 447

RESULT 12  
US-09-137-440-5  
Sequence 5, Application US/09137440  
Patent No. 624876  
GENERAL INFORMATION:  
APPLICANT: Barry, Gerard F.  
APPLICANT: Kishore, Ganesh M.  
APPLICANT: Padgett, Stephen R.  
APPLICANT: Scallings, William C.  
TITLE OF INVENTION: Glycophosphate Tolerant  
TITLE OF INVENTION: 5-Etholpyruvylshikimate-3-Phosphate Synthases  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF

STREET: 700 Chesterfield Village Parkway  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/137,440  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/833,485  
FILING DATE: 07-APR-1997  
APPLICATION NUMBER: US 08/306,063  
FILING DATE: 13-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,611  
FILING DATE: 28-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/576,537  
FILING DATE: 31-AUG-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoerner Jr., Dennis R.  
REGISTRATION NUMBER: 30,914  
REFERENCE/DOCKET NUMBER: 38-21(15117)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)737-6099  
TELEFAX: (314)737-6047  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 449 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-137-440-5

Query Match 83.1%; Score 1900.5; DB 3; Length 449;  
Best Local Similarity 82.9%; Pred. No. 2.4e-166;  
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

QY 1 MLGASSRPATARKSSGLSGTVRIIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
DB 1 MSHSASPRTARRESEALTEGIRIPGDKSISHRSFMFGGLASGETRITGLLEGEDVINTG 60  
QY 61 KAMQMGARIRKEGDTWIIDGVNGGLAPAPLDFGNAATGCRITMGLVGYDDSTFI 120  
DB 61 RAMQMGAKIRKEGDTWIIINGVNGCLQPEALDFGNAAGTARITMGLVGYDDSTFI 120  
QY 121 GPASLTGKPMGRVNLPLREMGVQVSEDDRLPVTLRGPKTPTPTTYRVPMASAOVKSAY 180  
DB 121 GPASLTGKPMGRVNLPLREMGVQVSEDDRLPVTLRGPKTPTPTTYRVPMASAOVKSAY 180  
QY 181 LLAGINTPGITTVIEPIIMTRDHTERKMLQGFANLIVETDADGVRTIRLEGRKLTGOVID 240  
DB 181 LLAGINTPGITTVIEPIIMTRDHTERKMLQGFANLIVETDADGVRTIRLEGRKLTGOVID 240  
QY 241 VPGDSSSTAFLVLAALVLEGSVITIRNVLMPRTGILITLOEMGADIEVLNARLAGGED 300  
DB 241 VPGDSSSTAFLVLAALVLEGSVITIRNVLMPRTGILITLOEMGADIEVLNARLAGGED 300  
QY 301 VADLVRSSLTGKGVVPPEDRAPSMIDEPILAVAAFAEGATVMNGLEELRYKESDRISA 360  
DB 301 VADLVRSSLTGKGVVPPEDRAPSMIDEPILAVAAFAEGATVMNGLEELRYKESDRISA 360  
QY 361 VANGKLINGVDCDEGETSLVVRGPDGKGLGNASGAATAVTHLDHRIAMSLVMGLVSENP 420  
DB 361 VANGKLINGVDCDEGETSLVVRGPDGKGLGNASGAATAVTHLDHRIAMSLVMGLVSENP 420  
QY 421 VTVDATMTATSPPEFMDLMAGLGAKIELS 450  
DB 421 VTVDATMTATSPPEFMDLMAGLGAKIELS 450

Db 418 VTDDSNMIATSFPEFMDMPGLGAKIELS 447

## RESULT 13

US-09-137-440-7  
Sequence 7, Application US/09137440  
Patent No. 6248876  
GENERAL INFORMATION:  
APPLICANT: Barry, Gerard F.  
APPLICANT: Kishore, Ganesh M.  
APPLICANT: Padgett, Stephen R.  
APPLICANT: Scallings, William C.  
TITLE OF INVENTION: Glycophate Tolerant  
TITLE OF INVENTION: 5-Etholpyruvylshikimate-3-Phosphate Synthases  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF  
STREET: 700 Chesterfield Village Parkway  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/137,440  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/833,485  
FILING DATE: 07-APR-1997  
APPLICATION NUMBER: US 08/306,063  
FILING DATE: 13-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,611  
FILING DATE: 28-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/576,537  
FILING DATE: 31-AUG-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoerner Jr., Dennis R.  
REGISTRATION NUMBER: 30,914  
REFERENCE/DOCKET NUMBER: 38-21(15117)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)737-6099  
TELEFAX: (314)737-6047  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 449 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-137-440-7

Query Match 83.1%; Score 1900.5; DB 3; Length 449;  
Best Local Similarity 82.9%; Pred. No. 2.4e-166;  
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

Db 1 MHHGSSRPATRKSSGSGTIRIPGDKSISHRSMFGLAGERTITLLEGEDVINTG 60  
1 MSHSASPRTARRESEALTGEIRIPGDKSISHRSMFGLAGERTITLLEGEDVINTG 60  
QY 61 KAMQAMGARIRKEGCTWIIDVNGGLAPAPLDFGNATGCRITMGLVGYDFDSPTI 120  
Db 61 RAMQAMGARIRKEGCTWIIDVNGGLAPAPLDFGNATGCRITMGLVGYDFDSPTI 120  
QY 121 GDASTKTRPMGVNLPLEMGVQVKSSEDDRLPVTIRGKPTPTPIYRVPMASAOVKSAY 180  
Db 121 GDASTKTRPMGVNLPLEMGVQVKSSEDDRLPVTIRGKPTPTPIYRVPMASAOVKSAY 180

QY 181 LLAGNTGCTTIVIEPIIMTRDHTERKLOFGANLTVETDADGRTIRLEGKLTGOVID 240  
Db 181 LLAGNTGCTTIVIEPIIMTRDHTERKLOFGANLTVETDADGRTIRLEGKLTGOVID 240  
QY 241 VGGDSSSTAFPLVAAALVPGSDVTLLNVLNMPRTGLITLLOEMGADIEVINPRLAGED 300  
Db 241 VGGDSSSTAFPLVAAALVPGSDVTLLNVLNMPRTGLITLLOEMGADIEVINPRLAGED 300  
QY 301 VADLVRSSSTLKGVTVPEDRAPSMIDEYPIILAVAAFPAGATVNMGLEELRYKESDRLSA 360  
Db 301 VADLVRSSSTLKGVTVPEDRAPSMIDEYPIILAVAAFPAGATVNMGLEELRYKESDRLSA 360  
QY 361 VANGKLNGVDDDEGETSLVVRGPRDGKLGAGAAVATHLDRIRMSFLVMGLVSENP 420  
Db 361 VANGKLNGVDDDEGETSLVVRGPRDGKLGAGAAVATHLDRIRMSFLVMGLVSENP 420  
QY 421 VTVDATMIATSFPEFMDMPGLGAKIELS 450  
Db 421 VTVDATMIATSFPEFMDMPGLGAKIELS 450  
QY 418 VTDDSNMIATSFPEFMDMPGLGAKIELS 447  
Db 418 VTDDSNMIATSFPEFMDMPGLGAKIELS 447

## RESULT 14

PCT-US91-06148A-5  
Sequence 5, Application PC/TUS9106148A  
GENERAL INFORMATION:  
APPLICANT: Barry, Gerard F.  
APPLICANT: Kishore, Ganesh M.  
APPLICANT: Padgett, Stephen R.  
TITLE OF INVENTION: Glycophate Tolerant  
TITLE OF INVENTION: 5-Etholpyruvylshikimate-3-Phosphate Synthases  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF  
STREET: 700 Chesterfield Village Parkway  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/06148A  
FILING DATE: 19910828  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/749,611  
FILING DATE: 28-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/576,537  
FILING DATE: 31-AUG-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoerner Jr., Dennis R.  
REGISTRATION NUMBER: 30,914  
REFERENCE/DOCKET NUMBER: 38-21(10535)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)537-6099  
TELEFAX: (314)537-6047  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 449 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US91-06148A-5

Query Match 83.1%; Score 1900.5; DB 5; Length 449;  
Best Local Similarity 82.9%; Pred. No. 2.4e-166;  
Matches 373; Conservative 32; Mismatches 42; Indels 3; Gaps 1;

Qy		I	MHGASSRPAATKRSGLSGTARIRGDSXISHRSMPFGLASGETRTGLLEGEDVNTG	60
Dd	1	MSSIASPKPATARRSRALTGEIRIPODXSISHSRMFGGLASGETRTGLLEGEDVNTG	60	
Qy		61	KAMQANGAIRKEGDWTIIDVGNGLLAPEALPDGNAATCGRLTMGLVGVDFDSTFI	120
Dd	61	RAMQANGAKIRKEGDWIIINGVNGCLLPEAALDPFNAGTGARLTWGLVTGYDMKTSFI	120	
Qy	121	GDA.S.LTKRMGRVLNLRBMGVOKSBOGDL.PYLRBPKTPPLTYRVPMASOVNSAV	180	
Dd	121	GDSLSIKRPGRVLNRBMGVQVEADDRMPLTLIPKIANPITYRVPMASOVNSAV	180	
Qy	181	LLAGLNPGLITVIIIEIMTRDHTEKMLOGFGANLTIVETDADGVSTRILERGKLTGVVID	240	
Dd	181	LLAGLNPGLITVIIIEVMTRDHTHEKMGFGADLVETDKDGVRHRIIRTGGKLVGTID	240	
Qy	241	VPEDBESTAFPLVAALLVPGSVTTILNLMTNTRIGLLILOENGADEIVNPNPLACGED	300	
Dd	241	VPEDBESTAFPLVAALLVBSDVTRIYNLMNPTRGILLILOENGADIEVNAPLACGED	300	
Qy	301	VADLRASSSTLKGVTVPEBDPASMDIEYILVAAPAFAEATVMNGLEELRKESDRLSA	360	
Dd	301	VADLRRAASKLKGVVPPERBASMDIEYVLAIAASPAGEIYVNDGDELRYKSDRLAA	360	
Qy	361	VANGLKLNVDCDEGETSLVVRGRPDGKLGNAASAVALATHLDHRIAMSFVWLVSBNP	420	
Dd	361	VARGLEANGVDCTEGEMSLTVRGRPDKGLG---GJVAITHLDHRIAMSFVWMLAEKP	417	
Qy	421	VTVDDATMTATSPEEFMDMAIGAKATEUS	450	
Dd	418	VTVDDSNMTATSPPEFMDMPGAGAKATEUS	447	

RESULT 15  
 PCT-US91-06148A-7  
 Sequence 7, Application PC/TUS9106148A  
 GENERAL INFORMATION:  
 APPLICANT: Barry, Gerard F.  
 APPLICANT: Kishore, Ganesh M.  
 APPLICANT: Padgett, Stephen R.  
 TITLE OF INVENTION: Glycosate Tolerant  
 TITLE OF INVENTION: 5-hydroxytryptamine-3-Phosphate Synthases  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B84F  
 STREET: 700 Chesterfield Village Parkway  
 CITY: St. Louis  
 STATE: Missouri  
 COUNTRY: USA  
 ZIP: 63198  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US91/06148A  
 FILING DATE: 19910828  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/749,611  
 FILING DATE: 28-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/576,537  
 FILING DATE: 31-AUG-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hoerner Jr., Dennis R.  
 REGISTRATION NUMBER: 30,914  
 REFERENCE/DOCKET NUMBER: 38-21(10535)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (314)537-6099  
 TELEFAX: (314)537-6047  
 INFORMATION FOR SEQ ID NO: 7:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US91-06148A-7

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Query Match	83.1%;	Score 1900.5;	DB 5;	Length 449;
Best Local Similarity	82.9%;	Pred. No. 2.4e-166;		
Matches 373;	Conservative 32;	Mismatches 42;	Indels 3;	Gaps 1;

Qy	1	MLHQAASRPATARKSSGLSGSVTR:PCGKSIISHRSFMEFGGLASGSTRITGLLEGEBVINTG	60
Db	1	MSHSAASKRPATARRSEALTEGIRIRPGKSIISHRSFMEFGGLASGSTRITGLLEGEDVINTG	60
Qy	61	KAMQAMGARIRKESDWTIIDVGNGGLLAPALPDFGNATGCLTMGLVGQYDPDSFI	120
Db	61	KAMQAMGAKIRKESDWTIINGVNGGCLLPAPALDPGNAAGTGLMGLVGTYYDMKTSFI	120
Qy	121	GDASLITRPMGRVYNLP:LRMGVOYKSESDGL:PYTLRGPKTPETRLTYRVPMASAOVKSAY	180
Db	121	GDASLSRPMGRVYNLP:LRMGVOYKSEADGDGRMPE:TLTGPKTANPEITTYRVPMASAOVKSAY	180
Qy	181	LLAGLNTPGITVTVIEPIPTRDHTKMLQGFGANLTVEITDADGVRTIRLEGKLTGVYID	240
Db	181	LLAGLNTPGVTTVIEPVWTRDHTKMLQGFADLTVEITDKGVHRIITGGOKLTGVQITD	240
Qy	241	VPGRPSTAPPLVAAALLVPGSDVITLLVNNPRTTGLITLQEBGADIEVINPRLAGED	300
Db	241	VPGRPSTAPPLVAAALLVPGSDVITIRVNNPRTTGLITLQEBGADIEVINARLAGGED	300
Qy	301	VADRVSSSTTKGTVPEDRAPSMIDEPIIAVAAAFAGATVNNNGLEELRVKESDRISA	360
Db	301	VADIRVPAASKLKGVVPPRRAPSMIDEPYLAIAASPRGEGTWDGDELKVKESDRILA	360
Qy	361	VANGIKINGVDCDEGETSLVVRGPRDGGKIGNAGAAVATLIDHRIAMSLVMGIWSEN	420
Db	361	VARGLEANGVDCTEGEMSLTVRGPRPDGGKIG---GGTAVATLIDHRIAMSLVMGIAAEKP	417
Qy	421	VTVDADTMIAATSPPEPMDIAMGAKTIELS	450
Db	418	VTVDSDNNIATSPPEPMDMMFGAKTIELS	447

Search completed: April 20, 2005, 15:24:34  
Job time : 51 secs

TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 7: